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SUMMARIES	AAW19282	AAW40350	AAB49478	AAW26384	AAW26382	AAW26381	AAW26385	AAW26383	AAW19283	AAB49479	AAW19281	AAW19616	AAY00737	AAB67416	AAB20221	AAB49471	AAR33708	AAR57327	AAY91117	AAB61792	AAY70323	AAY84058	AAY84060	AAY84059	AAE10625
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ALIGNMENTS

Job Howard Jack Antifungal protein, candida, fungal resistance, food additive, radish, crop protection, plant defensin, bacterial protection; preservative. Raphanus sativus antifungal protein 3 (Rs-AFP3). ¥. AAW19282 standard; protein; 50 (revised)
(first entry) 25-MAR-2003 21-JAN-1998 AAW19282; RESULT 1 AAW19282

96WO-GB003068. Raphanus sativus. WO9721815-A2 12-DEC-1996; 19-JUN-1997

(ZENE) ZENECA LTD.

95GB-00025455. 96GB-00006552.

13-DEC-1995; 28-MAR-1996;

WPI; 1997-332786/30. Meloen RH, Puij) Broekaert W, Sar Van Gelder WMJ;

Sijtsma L, Van Amerongen A; Borremans FAM, Rees SB;

Puijk WC, Schaaper WMM, , Samblanx GW, Fant F,

Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.

Disclosure; Fig 1; 65pp; English.

This protein sequence is the Rhapanus sativus (radish) mature antifungal protein (Rs-AFP3), which is homologous to proteins AAM19280- AAM19290. Shorter peptides, based on these proteins have been produced (see AAM19291-92, AAM19291-93, AAM19291-304, AAM19301-304, and AAM31765-834). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease

tolerance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct PI field.) 88888888

Sequence 50 AA;

Gaps ö 1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50 Length 50; ch 100.0%; Score 301; DB 2; Length 5 1 Similarity 100.0%; Pred. No. 6.3e-25; 50; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 50; Conserv 8

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AAW40350 standard; protein; 50 AA

AAW40350

(first entry) 23-JUN-1998 Radish Rs-AFP3 mature protein domain.

Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene; fungi; radish.

Raphanus sativus.

409800023-A2

38-JAN-1998

97WO-GB001672 20-JUN-1997;

96GB-00013753 01-JUL-1996;

(ZENE) ZENECA

Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM; Broekaert WF, Kazan K;

WPI; 1998-086663/08

Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.

Disclosure; Fig 1C; 72pp; English

This sequence represents the radish Rs-AFP3 mature protein domain which is used to explain a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fundi and does not require cytotoxic or potentially harmful chemicals

Sequence 50 AA;

Gaps ·, 100.0%; Score 301; DB 2; Length 50; 100.0%; Pred. No. 6.3e-25; Live 0; Mismatches 0; Indels 50; Conservative Local Similarity Query Match Best Loca Matches

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AAB49478 standard; protein; 50 AA AAB49478;

Radish antifungal protein Rs-AFP3

(first entry)

07-MAR-2001

Radish; antifungal; antimicrobial

Raphanus sativus.

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WO200071735-A1.

30-NOV-2000.

18-MAY-2000; 2000WO-GB001905.

99GB-00011933

21-MAY-1999;

(ZENE) ZENECA LID.

Greenland AJ, Fuentes Mateos AM,

WPI; 2001-041066/05.

Antimicrobial composition useful for treating microbial diseases in plants, comprises two antimicrobial agents, which are antifungal protein from Radish and Mirabilis of Impatiens.

Disclosure; Page 26; 29pp; English

The present sequence is an antifungal protein from Radish. This protein is useful for treating microbial diseases in plants and for inhibiting microbial growth in foodstuffs. In addition, the present sequence is useful for producing plants with improved resistance to microbial pathogens. The present protein can be used in conjunction with other antimicrobial proteins from Microbials (see AAB49472), and Impatiens (see AAB49474-B49477) to form an antimicrobial composition

Sequence 50 AA;

Gaps ô ch 100.0%; Score 301; DB 4; Length 50; Similarity 100.0%; Pred. No. 6.3e-25; 50; Conservative 0; Mismatches 0; Indels Query Match Best Local Matches 5

0;

RESULT 4 AAW26384

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AAW26384 standard; protein; 50 AA

AAW26384;

(first entry) 13-DEC-1997 Radish antifungal protein 2 mutant (delQ1,Q5M/P7S/K30G)

Rs-AFP2, radish antifungal protein 2; fungicide, salt tolerance; preservative, transgenic plant; crop protection.

Raphanus; sativus Synthetic.

0

Chimeric.

WO9721814-A1

19-JUN-1997

96WO-GB003065 12-DEC-1996;

RESULT 3 AAB49478

protein

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AW2331-90) are based on Rs-AFP2 and contain at least 1 mutation selected from a basic residue at positions 9 or 39, and a hydrophobic residue at positions 9 or 39, and a hydrophobic residue at positions 5 or 16. Proteins containing GlnSMet (see AAW36379), Gly9Arg (AAW26376), val39Arg (AAW26377) or Gly9Arg plus val39Arg (AAW26377) or Gly9Arg encoding Rs-AFP2 preprotein can be modified by recombinant DNA methods to allow expression of mutant isoforms in yeast as mating factor alpha 1 antifungal activity, especially when expressed in plant tissue where that may have curative as well as protective effects. They are useful for combating fungal diseases in agricultural, pharmaceutical or preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This polypeptide comprises a mutant isoform of radish antifungal protein (RB-AFP2) (see also AAM19616). Novel potent antifungal proteins (see AAW26371-90) are based on Rs-AFP2 and contain at least 1 mutation selected from a basic residue at positions 9 or 39, and a hydrophobic residue at positions 5 or 16. Proteins containing GlnSMet (see AAW26379), GINGNET (AAW26398), GIYAPARG (AAW26376), VA139ARG (AAW26377) or GIY9ARG plus Val39ARG (AAW26378) mutations are specifically claimed. A cDNA clone encoding Rs-AFP2 preprotein can be modified by recombinant DNA methods to
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                                                This polypeptide comprises a mutant isoform of radish antifungal
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                                                                                                                                                                                                                                                                                                                                                                                                           1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYRFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                       Score 294; DB 2; Length 50 Pred. No. 3.5e-24; 0; Mismatches 1; Indels
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              Disclosure; Page 4; 39pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rs-APP2, radish antifungal protein 2, fungicide, salt tolerance, ( ) preservative, transgenic plant; crop protection.
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Pred. No. 3.5e-24;
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allow expression of mutant isoforms in yeast as mating factor alpha I fusion proteins. The Rs-AFP2 mutants have enhanced salt tolerant antifungal activity, especially when expressed in plant tissue where that may have curative as well as protective effects. They are useful for combating fungal diseases in agricultural, pharmaceutical or preservative applications
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Pred. No. 5.7e-24;
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This polypeptide comprises a mutant isoform of radish antifungal protein 2 (Rs-AFP2) (see also AAW19616). Novel potent antifungal proteins (see AAW26311-96) are based on Rs-AFP2 and contain at least 1 mutation selected from a basic residue at positions 9 or 39, and a hydrophobic residue at positions 5 or 16. Proteins containing GlnSMet (see AAW26379), Gly9Arg (AAW26380), Gly9Arg (AAW26376), Val39Arg (AAW26377) or Gly9Arg plus Val39Arg (AAW26378) mutations are specifically claimed. A cDNA clone encoding Rs-AFP2 preprotein can be modified by recombinant DNA methods to allow expression of mutant isoforms in yeast as mating factor alpha 1 fusion proteins. The Rs-AFP2 mutants have enhanced salt tolerant may have curative as well as protective effects. They are useful for combating fungal diseases in agricultural, pharmaceutical or preservative
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                                                                                                                                                                                                                                        Rs-AFP2; radish antifungal protein 2; fungicide; salt tolerance;
preservative; transgenic plant; crop protection.
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                                1 KLCERSSGTWSGVCMNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
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   1 KLCERSSGTWSGVCGNNNACKNOCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 286; DB 2; Length 50; 96.0%; Pred. No. 2.5e-23; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 4; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AA
                                                                                                               AAW26383 standard; protein; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Broekaert WF, De Samblanx GW,
                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-GB003065
                                                                                                                                                                                                                                                                                                                                                                                                                                                    95GB-00025474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW19283 standard; protein;
                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-332785/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                           Raphanus; sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                       WO9721814-A1
                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-1996;
                                                                                                                                                                             13-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           applications
                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-1997.
                                                                                                                                                                                                                                                                                                        Synthetic.
Chimeric.
                                                                                                                                               AAW26383;
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Best Local S
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ID AAW1
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                                                                                  RESULT 8
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Antimicrobial composition useful for treating microbial diseases in plants, comprises two antimicrobial agents, which are antifungal protein from Radish and Mirabilis of Impatiens.
                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is an antifungal protein from Radish. This protein is useful for treating microbial diseases in plants and for inhibiting microbial growth in foodstuffs. In addition, the present sequence is useful for producing plants with improved resistance to microbial pathogens. The present protein can be used in conjunction with other antimicrobial proteins from Mirabilis (see AAB49473), and mimicrobial composition forms an antimicrobial composition
                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 26; 29pp; English.
                                                                                                                                                                                                           Fuentes Mateos AM;
                                                                                                                                         99GB-00011933.
                                                                                                        18-MAY-2000; 2000WO-GB001905.
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                                                                                                                                                                                                                                              WPI; 2001-041066/05.
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   Raphanus sativus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Van Gelder WMJ;
                                    WO200071735-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51 AA;
                                                                                                                                                                        (ZENE ) ZENECA
                                                                                                                                                                                                           Greenland AJ,
                                                                                                                                         21-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9721815-A2
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                                                                     30-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW19281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This protein sequence is the Raphanus sativus (radish) mature antifungal protein (Rs-AFP4), which is homologous to proteins AAM19280- AAM19290. Shorter peptides, based on these proteins have been produced (see AAM19291-92, AAM19294-98, AAM19301-304, AAM193030-34 and AAM31765-834). Plants containing DNA sequences encoding these proteins have improved control fungion to bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorgable of expressing the peptide into the soil. (Updated
                                                                                                                     Antifungal protein; candida; fungal resistance; food additive; radish; crop protection; plant defensin; bacterial protection; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Sijtsma L, Van Amerongen A;
Borremans FAM, Rees SB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 282; DB 2; Length 51;
Pred. No. 6.7e-23;
3; Mismatches 2; Indels
                                                                                    Raphanus sativus antifungal protein 4 (Rs-AFP4).
                                                                                                                                                                                                                                                                                                                                                                                                  Schaaper WMM,
GW, Fant F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on 25-MAR-2003 to correct PI field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Radish; antifungal; antimicrobial.
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                                                                                                                                                                                                                                                                               96WO-GB003068
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96GB-00006552.
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                                  (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                    Meloen RH, Puijk WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-332786/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                        Raphanus sativus.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Gelder WMJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51 AA;
                                                                                                                                                                                                           WO9721815-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  Broekaert W,
                                                                                                                                                                                                                                                                               12-DEC-1996;
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28-MAR-1996;
                                25-MAR-2003
21-JAN-1998
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AAW19283;
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Antifungal protein, candida, fungal resistance, food additive, radish, crop protection, plant defensin, bacterial protection, preservative.
                                                           Gaps
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Samblanx GW, Fant F, Borremans FAM, Rees SB;
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                                                                                                                                                         2 KLCERSSGTWSGVCGNNNACKNQCINLEGARHGSCNYIFPYHRCICYFPC 51
                                                                                                                    1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
   Length 51;
Match 93.7%; Score 282; DB 4; Length 51 Local Similarity 90.0%; Pred. No. 6.7e-23; Local Similarity 93; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raphanus sativus antifungal protein 2 (Rs-AFP2)
                                                                                                                                                                                                                                                                                                                                AAW19281 standard; protein; 51 AA
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Disclosure; Fig 1; 65pp; English
                                                                                              46; Conservative
                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                       Raphanus sativus
                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                   Misc-difference
                                                                                Sequence 51 AA;
                                                                                                                                                                                                                                                              (ZENE ) ZENECA
                                                                                                                                                                                                                                                                      Broekaert WF,
                                                                                                                                                                                                                                 WO9721814-A1
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                                                                                                                                              13-DEC-1997
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                                                                                                                                       AAW19616;
                                                                                              Matches
                                                                                                                        RESULT 12
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This polypeptide comprises radish antifungal protein 2 (Rs-AFP2). Novel potent antifungal proceins (see AAW26371-90) based on Rs-AFP2 contain at least 1 mutation selected from a basic residue at positions 9 or 39, and a hydrophobic residue at positions 5 or 16. Proteins containing Gln5Met (see AAW26379), Gly16Met (AAW26300), Gly2Arg (AAW26376), val39Arg (AAW26377) or Gly9Arg plus val39Arg (AAW26377) mutations are specifically claimed. A cDNA clone encoding Rs-AFP2 preprotein can be modified by recombinant DNA methods to allow expression of mutant isoforms in yeast as mating factor alpha 1 fusion proteins. The Rs-AFP2 mutants have enhanced salt tolerant antifungal activity, especially when expressed in plant tissue where that may have curative as well as protective effects. They are useful for combating fungal diseases in agricultural, pharmaceutical or preservative applications This sequence represents an antifungal peptide. The invention relates to an antifungal composition comprising one or more antifungal agents and one or more food additives, providing that the composition dees not contain nicin or lactoferrin or a derivative, trichorziamine or lysozyme, the relative amounts of antifungal agent and food additive being such that they enhance the activity of the overall antifungal activity of the composition. Especially the antifungal agent is derived from a plant or Food additive synergistically enhances activity of an antifungal agent especially for prevent food and beverage spoilage. New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents. 1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 2 KLCQRPSGTWSGVCGNNNACKNQCIRLEKARHGSCNYVFPAHKCICYFPC Score 281, DB 2, Length 51, Pred. No. 8.6e-23, 2; Mismatches 2, Indels Antifungal agent; food additive; food spoilage prevention. Ā Greenland AJ, Fuentes Mateos AM AAY00737 standard; peptide; 51 Claim 15; Fig 7; 40pp; English. Claim 1; Fig 1; 39pp; English 98WO-GB002010. 93.4%; 97GB-00014564 (first entry) Antifungal peptide RSAFP2 1 Similarity 92.0 46; Conservative WPI; 1999-120402/10. WPI; 1997-332785/30. (ZENE) ZENECA LTD. Sequence 51 AA; 14-MAY-1999 WO9902038-A1 09-JUL-1998; 10-JUL-1997; 21-JAN-1999. Synthetic AAY00737; Query Match Best Local S Matches RESULT 13 AAY00737 8 dd This protein sequence is the Rhapanus sativus (radish) mature antifungal protein (Rs-AFP2), which is homologous to proteins AAM19280. AAM19290. Shorter peptides, based on these proteins have been produced (see AAW19291-92, AAW19294-98, AAW19101-304, AAM19310-34 and AAW131765-834). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, they may also have curative as well as protective actions. The peptides to plants they may also have curative as well as protective actions. The peptides in croorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct PI field.) ö Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent. /note= "Val at position 39 may be replaced by a basic amino acid, preferably Arg"" Gaps /note= "Gly at position 9 may be replaced by a basic amino acid, preferably Arg"" Rs-AFP2; radish antifungal protein 2; fungicide; salt tolerance; preservative; transgenic plant; crop protection. . 0 1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50 /note= "Gly at position 16 may be replaced by hydrophobic amino acid, preferably Met" 39 /note= "Gln at position 5 may be replaced by hydrophobic amino acid, preferably Met"" 2 KLCQRPSGTWSGVCGNNNACKNQCIRLEKARHGSCNYVFPAHKCICYFPC 93.4%; Score 281; DB 2; Length 51; 92.0%; Pred. No. 8.6e-23; ive 2; Mismatches 2; Indels Radish antifungal protein 2 (Rs-AFP2). Location/Qualifiers AAW19616 standard; protein; 51 AA De Samblanx GW, 96WO-GB003065 (first entry)

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Gaps

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seed and the food additive is selected from an acid, salt or ester or a 1 dec alkyl ether or derivatives. The compositions are useful in preventing food spoilage e.g. in a wide range of foods and beverages including fruits, jams and dairy products, caused by the spoilage organisms fruits, jams and dairy products, caused by the spoilage organisms hastainum, Penicallium chrysogenum, P. roquefortli, P. nalgiovense, P. commune, Alternaria sp., Cladosporum sp., Tichoderma harzianum, Mucor plumbeus, Aspergillus versicolor and Scopulariopsis brevicaulis. The food additive and antifungal agent act synergistically to enhance the overall antifungal activity of the composition to a level above the sum of each single component
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptide for combating bacterial infections, comprises modified cysteine residues, modified by addition, substitution or deletion to block their ability to form disulfide bridges.
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                                                                                                                                                                                                                                                                                                                                                                                         2 KLCQRPSGTWSGVCGNNNACKNQCIRLEKARHGSCNYVFPAHKCICYFPC
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                                                                                                                                                                                                                                                                          Score 281; DB 2; Length 51;
Pred. No. 8.6e-23;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Van Amerongen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of the plant defensin Rs-AFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schaaper WMM, Sijtsma L,
Rees SB, Osborn RW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB67416 standard; protein; 51 AA
                                                                                                                                                                                                                                                                              93.4%;
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Borremans FAM, Rees SB,
                                                                                                                                                                                                                                                                                                                         46; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                      Sequence 51 AA;
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Val, Leu, Phe, His in antimicrobial protein/peptide of
Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "optionally substituted by Trp in antimicrobial protein/peptide of Claim 1"
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protein/peptide of Claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "optionally substituted by Leu, Ile, Trp, Phe,
Met, Lys, Arg, Tyr or His in antimicrobial
protein/peptide of Claim 1"
                                                              Gaps
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                                                                                                                                                                                                                                                                                          Radish; defensin; Rs-AFP2; antimicrobial; antifungal; fungicide;
transgenic plant; disease resistance; infection; therapy.
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                                                                                                                51
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                                                                                                         1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                     Length 51;
                                    Score 281; DB 4;
Pred. No. 8.6e-23;
2; Mismatches 2;
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                                      93.4%;
92.0%;
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                                                               46; Conservative
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15..36
21..45
25..47
                                                   Similarity
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Misc-difference 32
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            Sequence 51 AA;
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Disulfide-bond
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                                     Query Match
Best Local S:
Matches 46
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Sijtsma L,
31-JUL-2000; 2000WO-GB002941.
                              99GB-00018155.
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                                                                                                                                          WPI; 2001-182938/18.
                                                             (ZENE ) ZENECA LTD.
                                                                                           Posthuma GA,
Borremans FAM;
                              02-AUG-1999;
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Van Amerongen A,

Novel antimicrobial proteins derived from plant defensin useful against a broad spectrum of microbes, comprise substitutions at specified portions of its sequence.

Disclosure; Page 6; 64pp; English

The present sequence is that of radish defensin protein Rs-AFP2. A claimed antimicrobial protein or peptide is derived from a plant defensin characterised by having 1 or more replacement amino acids, as indicated at positions 32, 34, 35, 36, 37, 38, 39, 40, 41 and/or 42 of the Rs-AFP2 sequence, provided that the replacement amino acids are not found raturally at these positions and the protein does not comprise only a replacement arginine at position 37, 39 or 42. In addition, cysteine replacement arginine at position 37, 39 or 42. In addition, cysteine replacement arginine at position 37, 39 or 42. In addition, cysteine replacement arginine at position 37, 39 or 42. In addition, cysteine replacement arginine at position 37, 39 or 42. In addition, cysteine replacement arginine at position 37, 39 or 42. In addition, cysteine replacement by a lapha-aminobutyric acid. The antimicrobial protein or peptide can be used on its cown, or in syneatistic combination with a plant defensin, to combat fungi. A plant having improved resistance to a fungal or microbial pathogen can contain recombinant DNA which expresses a clamed antimicrobial protein or peptide. The claimed antimicrobial protein or peptide is also used as a pharmaceutical to treat or prevent a microbial infection, especially a fungal infection (all claimed)

Sequence 51 AA;

Gaps · 0 93.4%; Score 281; DB 4; Length 51; 92.0%; Pred. No. 8.6e-23; tive 2; Mismatches 2; Indels Query Match Best Local Similarity 92.09 Matches 46; Conservative

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Search completed: May 11, 2004, 16:56:27 Job time : 55 secs

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1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36, Application US/09077948A Patent No. 6605698 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De Samblanx, Genoveva
Sitifema, Lolke
Meloen, Robbert
Puijk, Wouter
Schaaper, Wilhelmus
Broekaert, Willem
Van Gelder, Wilhelmus
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les 50; Conserv
RESULT 2
US-09-077-948A-36
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APPLICANT:
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Sequence 69,
Sequence 11,
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Sequence 67,
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1 KLCERSSGTWSGVCGNNNAC......QHGSCNYVFPAHKCICYFPC
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-077-951-20

US-09-077-951-20

US-09-077-951-20

US-09-077-951-20

US-09-077-951-37

US-09-08-77-19-59

US-08-777-19-59

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US-08-656-318A-3
US-08-627-706-18
US-08-777-192-19
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Maximum Match 100%
Listing first 45 summaries
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100.0%; Pred. No. 6.5e-26;
tive 0; Mismatches 0;
US-08-956-459-3

US-08-971-982-19

US-09-077-951-8

US-09-077-951-8

US-09-077-948A-34

US-09-077-948A-34

US-09-077-948A-34

US-09-777-948A-34

US-08-777-192-49

US-08-777-192-49

US-08-977-192-49

US-08-977-982-49

US-09-077-951-22

US-09-077-951-65

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US-09-077-951-65

US-09-077-951-65

US-09-077-951-65

US-09-077-951-65
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: De Samblanx, Genoveva
APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
TILE OF INVENTION: Antifungal Proteins
FILE REFERENCE: PPD50093
CURRENT APPLICATION NUMBER: US/09/077,951
CURRENT APPLICATION NUMBER: US/09/077,951
CURRENT FILING DATE: 1999-03-11
FARLIER FILING DATE: 1996-12-13
BARLIER FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PARCHILLY DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PARCHILLY DATE: 1996-12-12
                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                         ; Sequence 10, Application US/09077951; Patent No. 6372888; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Raphanus sativus
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                                                                                                                                                                                                                                           ; DB 4; Length 50; 3.7e-25;
                                                                                                                                                                                                                                              Score 294; DB
Pred. No. 3.7e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Broekaert, Willem
APPLICANT: Broekaert, Willem
APPLICANT: Broekaert, Willem
APPLICANT: Rese, Sarch
TILE OF INVENTION: Antifungal Proteins
FILE REFERENCE: PPD5003
CURRENT APPLICATION WUMBER: US/09/077,951
CURRENT APPLICATION NUMBER: GB 9525474.4
EARLIER APPLICATION NUMBER: PCT/GB96/03065
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: De Samblanx, Genoveva
APPLICANT: De Samblanx, Genoveva
APPLICANT: Brockaert, Willem
APPLICANT: Reces, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REPERENCE: PPD50093
CURRENT APPLICATION NUMBER: US/09/077,951
CURRENT FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: PCT/GB96/03065
BARLIER FILING DATE: 1996-12-13
BARLIER FILING DATE: 1996-12-13
SARLIER FILING DATE: 1996-12-12
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 71
LENGTH: 50
TYPE: PRT
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     PCT/GB96/03065
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Patent No. 6372888
GENERAL INFORMATION:
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; Sequence 71, Application US/09077951
; Patent No. 6372888
EARLIER APPLICATION NUMBER: PCT/
EARLIER FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 70
LENGTH: 50
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.0%;
Matches 49; Conservative
                                                                                                                                              TYPE: PRT;
CRGANISM: Raphanus sativus
US-09-077-951-70
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, ORGANISM: Raphanus sativus
US-09-077-951-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 68, Application US/09077951
; Sequence 68, Application US/09077951
; Parent No. 6372888
; GENERAL INFORMATION:
    APPLICANT: De Samblanx, Genoveva
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; TILE REPERENCE: PDP50093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT APPLICATION NUMBER: GB 9525474.4
EARLIER APPLICATION NUMBER: PCT/GB96/03065
EARLIER PILING DATE: 1995-12-13
EARLIER PILING DATE: 1995-12-13
EARLIER PILING DATE: 1995-12-13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 68
LENGTH: 50
FILE REFERENCE: 109846-257 (SYN-035)
CURRENT APPLICATION WUMBER: US/09/077,948A
WINDERT FILING DATE: 1998-08-07
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1996-02-12
PRIOR FILING DATE: 1996-03-28
PRIOR PILING DATE: 1996-03-28
PRIOR PILING DATE: 1996-03-28
PRIOR PILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-03-28
SOFTWARE: PEASEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
ENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaert, Willem
APPLICANT: Broekaert, Millem
TITLE OF INVENTION: Antifungal Proteins
FILE REPERENCE: PPD5.0093
CURRENT FILING DAFE: 1999-03-11
CURRENT FILING DAFE: 1999-03-11
EBALIER APPLICATION NUMBER: GB 9525474.4
EBALIER FILING DATE: 1999-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 70, Application US/09077951
Patent No. 6372888
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Raphanus sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Raphanus sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          US-09-077-948A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-077-951-68
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Query Match Matches

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2 KLCERSSGTWSGVCGNNNACKNQCINLEGARHGSCNYIFPYHRCICYFPC 51
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 109846-257(SYN-035)
FILE REFERENCE: 109846-257(SYN-035)
CURRENT APPLICATION WUMBER: US/09/077,948A
CURRENT APPLICATION WUMBER: US/09/077,948A
FRIOR APPLICATION NUMBER: PCT/(CB96/03068
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-03-28
SRIOR FILING DATE: 1995-11-13
WUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                Sequence 37, Application US/09077948A, Patent No. 6605698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08656318A, Patent No. 2750504; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             De Samblanx, Genoveva
Sititema, Lolke
Meloen, Robbert
Puijk, Wouter
Schaeper, Wilhelmus
Broekaert, Willem
Van Gelder, Wilhelmus
                                                                                                                                                                                                                  Van Amerongen, Aart
Fant, Franky
                                                                                                                                                                                                                                                             Borremans, Frans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Raphanus sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sarah
                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                 US-09-077-948A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-077-948A-37
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                     1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
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                                                               Score 292; DB 4; Length 50;
Pred. No. 6e-25;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 286; DB 4;
Pred. No. 2.7e-24;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                     APPLICANT: De Samblanx, Genoveva
APPLICANT: De Samblanx, Genoveva
APPLICANT: Brockaert, Willem
APPLICANT: Brockaert, Willem
TITLE OF INVENTION: Antifungal Proteins
FILE REPRENCE: PPD50093
CURRENT APPLICATION NUMBER: US/09/077,951
CURRENT FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: GB 9525474.4
EARLIER PLING DATE: 1995-12-13
SARILER FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PALENT VONS: 77
LENGTH: 50
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: De Samblanx, Genoveva
APPLICANT: De Samblanx, Genoveva
APPLICANT: Brockaert, Willem
APPLICANT: Rees, Sarah
ITILB OF INVENTION: Antifungal Proteins
FILE REFERENCE: PPDS0093
CURRENT APPLICATION NUMBER: US/09/077, 951
CURRENT FILING DATE: 1999-03-11
FARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1996-12-13
EARLIER FILING DATE: 1996-12-12
NUMBER: OF SEQ ID NOS: 77
                                                                                                                                                                                                                                                                               US-09-077-951-69
; Sequence 69, Application US/09077951
; Patent No. 6372888
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Patent No. 6372888
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ilarity 96.0%;
Conservative
                                                               Query Match
Best Local Similarity 98.0%;
Matches 49; Conservative
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SEQ ID NO 11
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Raphanus sativus
US-09-077-951-11
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Best Local Similarity 90.0°
Matches 45; Conservative
; ORGANISM: Raphanus sativus
US-09-077-951-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Raphanus sativus
US-09-077-951-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
hes 48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                      2 KLCERSSGTWSGVCGNNNACKNQCINLEGARHGSCNYIFPYHRCICYFPC 51
                                                                                                           1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
Query Match 93.7%; Score 282; DB 4; Length 51; Best Local Similarity 90.0%; Pred. No. 7.4e-24; Matches 45; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSE: Intellectual Property Group of STREET: 1100 New York Avenue, N.W. CITY: Washington CITY: Washington COUNTRY: U.S.A. COUNTRY: U.S.A. ZIP: Z1005-3918
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, RUPERT W.
APPLICANT: REES, SARAH B.
TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
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SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 92.0
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN...
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-627-706-19
                                                                                                                                                                   Query Match
Best Local Similarity
Matches 46; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-08-956-459-4
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US-08-672-706-19

| Sequence 19 Application US/08627706
| Patent No. 5773696
| Patent No. 5773696
| GENERAL INFORMATION:
| APPLICANT: Liang, Jihong
| APPLICANT: Liang, Jihong
| APPLICANT: Rosenberger, Cindy A.
| APPLICANT: Rosenberger, Cindy A.
| TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
| VUMBER OF SEQUENCES: 19
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
| STREET 700 Chesterfield Village Parkway No. 5773696th
| CITY: St. Louis
| STATE: Missouri
| COUNTRY: USA
| ZIP: 63198
| COMPUTER PITTER
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 281; DB 1; Length 51;
Pred. No. 9.4e-24;
2; Mismatches 2; Indels
                                                              CLASSIFICATION: evv
PRIOR APPLICATION: evv
PRIOR APPLICATION NUMBER: GB 9326424.0
FILING DATE: 24-DEC-1993.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/02766
FILING DATE: 19-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 224199/SEB37925/UST
TELEPOMINICATION INFORMATION:
TELEPOMINICATION INFORMATION:
TELEPOMIS: (202) 861-3075
TELEPAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERIETICS:
LENGTH: 51 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706 PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEPHONE: (314)537-6047
INFORMATION FOR SEQ ID NO: 19:
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,318A
FILING DATE: 12-JUN-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 92.0%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RS-AFP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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ORGANISM:
US-08-656-318A-4
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Gaps
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                                                                                                                                                                                                           1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
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ch 93.4%; Score 281; DB 1; Length 51; 1. Similarity 92.0%; Pred. No. 9.4e-24; 46; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elby PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,459
FILING DATE: 22-OCT-1996
CLASSIFFCATION: 80
FILING DATE: 12-UVN-1996
FILING DATE: 12-UVN-1996
FILING DATE: 12-UVN-1996
FILING DATE: 13-DEC-1994
FILING DATE: 19-DEC-1994
FILING DATE: 24-DEC-1993
FILING DATE: 24-DEC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08956459
Patent No. 5919918
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: GANNUE, BRUNO P. A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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Search completed: May 11, 2004, 16:59:12 Job time: 42 secs
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-951-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Raphanus sativus
US-09-077-951-20
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Best Local Similarity
                                                                                  Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: W. Yonnie S.
APPLICANT: W. Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.4%; Score 281; DB 3; Length 51; 92.0%; Pred. No. 9.4e-24; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                         ZIR: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: DATE C compatible
CORPARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION WUMBER: US/09/103,489
FILING DATE: 24-UUN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34.56
REFERENCE/DOCKET NUMBER: 38-21 (10700) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-624
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-09-077-951-9
Sequence 9, Application US/09077951
Sequence 9, Application US/09077951
Sequence 9, Application US/09077951
Sequence 9. Application US/09077951
GENERAL INFORMATION:
APPLICANT: Broekaert, Willem
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: PDE0093
CURRENT APPLICATION NUMBER: US/09/077,951
CURRENT FILING DATE: 1999-03-11
EARLIER FILING DATE: 1995-12-13
EARLIER PRILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.0
SENGIB NO 9
LENGIH: 51
                       US-09-103-489-19
; Sequence 19, Application US/09103489
; Patent No. 6215048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 92.0
Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                1 KLCERSSGTWSGVCGNNNACKNOCIRLEGAQHGSCNYVFPAHKCICYFPC
       Length 51;
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                                                 2; Indels
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ilarity 92.0%; Pred. No. 9.4e-24;
Conservative 2; Mismatches 2;
93.4%; Score 281; DB 4;
illarity 92.0%; Pred. No. 9.4e-24;
Conservative 2; Mismatches 2;
                                                                                                                                                                                                            RESULT 15
US-09-077-951-20

i Sequence 20, Application US/09077951
i Sequence 20, Application US/09077951
i Patent No. 637288
i GENERAL INFORMATION:
i APPLICANT: Be Samblanx, Genoveva
i APPLICANT: Rees, Sarah
i TITLE OF INVENTION: Antifungal Proteins
i FILE REFRENCE: PPD5003
i CURRENT APPLICATION NUMBER: US/09/077,951
CURRENT APPLICATION NUMBER: GB 9525474.4
i EARLIER APPLICATION NUMBER: GB 9525474.4
i EARLIER PILING DATE: 1995-12-13
i EARLIER PILING DATE: 1995-12-13
i EARLIER PILING DATE: 1996-12-12
i NUMBER OF SEQ ID NOS: 77
i SOFTWARE: PatentIN Ver. 2.0
i ERNOTH: SA
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Sequence 37, Appl Sequence 77, Appl Sequence 14, Appl Sequence 21, Appl Sequence 21, Appl Sequence 19, Appl Sequence 18, Appl Sequence 24, Appl Sequence 22, Appl Sequence 35, Appl Sequence 20, Appl Sequence 22, Appl Sequence 55, Appl Sequence 55, Appl Sequence 65, Appl

ALIGNMENTS

Sequence 75, Appl Sequence 17, Appl Sequence 23, Appl

Sequence 65, 7 Sequence 31, 8 Sequence 39, 8 Sequence 44, 8

Sequence 73, Sequence 28, Sequence 41, Sequence

> ZIP: 19850
>
> COMPUTER READABLE FORM:
> MEDIUM TYPE: Floppy disk
> COMPUTER: IBM PC compatible
> OPERATING SYSTEM: PC-DOS/MS-DOS
> SOPTWARS: Patentin Release #1.0, Version #1.25
> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: US/09/732,561 GENERAL INCORANTION:
> APPLICANT: Thomma, Bart
> APPLICANT: Thomma, Bart
> APPLICANT: Terras, Franky
> APPLICANT: Penninck, Iris
> APPLICANT: Manners, John
> APPLICANT: Manners, John
> APPLICANT: Macan, Kemal
> APPLICANT: Brockeert, Willem
> ITITE OF INVENTION: Plant Protection Method
> NUMBER OF SEQUENCES: 24
> CORRESPONDENCE ADDRESS:
> ADDRESSEE: ZEBECA AG Products
> STREET: Milmington FILING DATE:
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: PCT/GB97/01672
> FILING DATE: 20-JUN-1997
> ATTORNEY/AGENT INPORMATION:
> NAME: Hohenschutz, Liza D.
> REGISTRATION NUMBER: 33,712 FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/202,638 FILING DATE: Sequence 20, Application US/09732561 Patent No. US20020035738A1

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                       APPLICANT:
APPLICANT:
APPLICANT:
Rees, Sarah
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 09/077,951
PRIOR APPLICATION NUMBER: 1996-06-10
PRIOR FILING DATE: 1996-12-13
SOFTWARE: PATCH ONCS: 77
SOFTWARE: PATCH ONCS: 77
SOFTWARE: PATCH ONCS: 77
SOFTWARE: PATCH ONCS: 77
LENGTH: 50
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Sequence 68, Application US/10006252A

Publication No. US20020152498A1

GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Antifungal Proteins
FILE REFRENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT PPLICATION NUMBER: US/10/006,252A
CURRENT PLING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR APPLICATION NUMBER: PCT/GB96/03065
PRIOR APPLICATION NUMBER: PCT/GB96/03065
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-12

NUMBER: OF SEQ ID NOS: 77

SEQ ID NO 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Raphanus sativus
US-10-006-252A-10
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Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 301; DB 9; Length 50; Best Local Similarity 100.0%; Pred. No. 9.2e-27; Matches 50; Conservative 0; Mismatches 0; Indels
REFERENCE/DOCKET NUMBER: PPD 50165/UST

TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699

INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: Inhear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: RS-AFP3
US-09-732-561-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Van Amerongen, Aart
APPLICANT: Fant, Franky
APPLICANT: Borremans, Frans
APPLICANT: Borremans, Frans
APPLICANT: Schaaper, Lolke
APPLICANT: Schaaper, Wilhelmus
APPLICANT: Schaaper, Wilhelmus
APPLICANT: Phijk, Wouter
APPLICANT: Schaaper, Wilhelmus
APPLICANT: Breekaert, Willem
APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
TITLE OF INVENTION: Antifungal Proteins
TITLE FREEBRICE: 2003-40-13
CURRENT APPLICATION NUMBER: US/10/388,361A
CURRENT FILING DATE: 1998-00-07
PRIOR APPLICATION NUMBER: US/09/077,948
PRIOR APPLICATION NUMBER: GB 960655.9
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-12-12
PRIOR APPLICATION NUMBER: GB 9525455.3
PRIOR FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 141
SCOTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application US/10388361A Publication No. US20030226169A1 GENERAL INFORMATION:
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CRGANISM: Raphanus sativus
US-10-388-361A-36
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RESULT 3
US-10-006-252A-10
IS-quence 10, Application US/10006252A
Publication No. US20020152498A1
GENERAL INFORMATION:

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Pred. No. 9.5e-26;
0; Mismatches 1;
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95.0%; Score 286; DB 13;
Best Local Similarity 96.0%; Pred. No. 4.5e-25;
Matches 48; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 69, Application US/10006252A

| SENERAL INFORMATION:
| Publication No. US200201524981|
| GENERAL INFORMATION:
| APPLICANT: De Samblanx, Genoveva
| APPLICANT: Broekaert, Willem
| APPLICANT: Broekaert, Willem
| APPLICANT: Broekaert, Willem
| TITLE OF INVENTION: Antifungal Proteins
| TITLE OF INVENTION: Antifungal Proteins
| TITLE OF INVENTION: ANTIGUARD NOTO:
| FILE REFERENCE: SYN-034DV
| CURRENT FILING DATE: 1998-06-10
| PRIOR FILING DATE: 1998-06-10
| PRIOR FILING DATE: 1998-06-10
| PRIOR FILING DATE: 1998-12-13
| PRIOR FILING DATE: 1996-12-12
| NUMBER OF SEQ ID NOS: 77
| SOFTWARE: PATENTIN VET: 2.0
| SEQ ID NO 69
| SEQ ID NO 69
         CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/077,951
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR PILING DATE: 1995-12-13
PRIOR FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOSTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borremans, Frans
De Samblanx, Genoveva
Sititsma, Lolke
Meloen, Robbert
Puijk, Wouter
Schaaper, Wilhelmus
BrockAert, Willem
                                                                                                                                                                                                                                                                                                                                                97.0%;
98.0%;
                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Raphanus sativus
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US-10-006-252A-69
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Best Local Similarity 98.0
Matches 49; Conservative
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US-10-006-252A-69
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                         97.7%; Score 294; DB 13; Length 50; 98.0%; Pred. No. 5.7e-26; Live 0; Mismatches 1; Indels
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Pred. No. 7.3e-26;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No. US20020152498A1
GENERAL INFORMATION:
APPLICANT: Beambarx, Genoveva
APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
ITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN-034DV NUMBER: US/10/006,252A
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 2001-12-04
PRIOR PILING DATE: 2098-06-10
PRIOR FILING DATE: 1998-12-13
PRIOR FILING DATE: 1998-12-13
PRIOR FILING DATE: 1995-12-13
PRIOR FILING DATE: 1995-12-13
PRIOR FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENTIN VET. SO
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/077,951
PRIOR APPLICATION NUMBER: 09/077,951
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-12-13
PRIOR FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENT OFF: 1996-12-12
NUMBER OF SEQ ID NOS: 77
LENGTH: 50
LENGTH: 50
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FILE REFERENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
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APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
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; ORGANISM: Raphanus sativus
US-10-006-252A-70
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ORGANISM: Raphanus sativus
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Best Local Similarity
Matches 49; Conservat
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Matches 49; Conserv
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US-10-006-252A-71
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Pred. No. 1.3e-24;
3; Mismatches 2;
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Publication No. US20020152498A1
GENERAL INFORMATION:
APPLICANT: Brockaert, Willem
APPLICANT: Brockaert, Willem
APPLICANT: Brockaert, Willem
APPLICANT: Brockaert, Willem
APPLICANT: Rese, Sarah
FILE REFERENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR FILING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: GB 9525476.5
PRIOR FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENTING UNIVER: PCT/GB96/03065
NUMBER OF SEQ ID NOS: 77
LENGTH: 51
                                                                                  CURRENT APPLICATION NUMBER: US/10/388,361A
CURRENT FILING DATE: 2003-03-13
PRIOR APPLICATION NUMBER: US 09/077,948
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1998-12-12
PRIOR APPLICATION NUMBER: PCT/GB96/03068
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FSELSEQ for Windows Version 4.0
SOFTWARE: 51
                 APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: 50094PPDDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 19, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
Van Gelder, Wilhelmus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.0%;
Matches 45; Conservative
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Best Local Similarity 90.0%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Raphanus sativus US-10-388-361A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Raphanus sativus US-10-006-252A-11
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Sequence 19, Application US/10681972
; Sequence 19, Application US/20040064850A1
; Publication No. US20040064850A1
; Publication No. US20040064850A1
; GENERAL INFORMATION:
    APPLICANT: Liang, Ulhong
    APPLICANT: Shab, Dilip M.
    APPLICANT: Rosenberger, Cindy A.
    APPLICANT: Rosenberger, Cindy A.
    APPLICANT: Rosenberger, Cindy A.
    APPLICANT: Rosenberger, Cindy A.
    APPLICANT: NOWERLER PROPERTY OF THE OF INVENTION: Plant Pathogenic Fungi
    TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control
    TITLE OF INVENTION: Dlant Pathogenic Fungi
    TITLE OF INVENTION: NUMBER: US/09/829,381D
    PRIOR APPLICATION NUMBER: US/09/829,381D
    PRIOR APPLICATION NUMBER: 09/103,489
    PRIOR PILING DATE: 1998-06-24
    NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
COUNTR: MSA
ZIP: 63198
COMPUTER READABLE FORM:
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Wu, Yonnie S.
Rosenberger, Cindy A.
ROSENDERION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOUER KEALDED FOWD

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPATION SYSTEM: PC-DOS/MS-DOS

SOFWRARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 09-Apr-2001

CLASSIFICATION: <university of the compatible of the
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; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-829-381A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cohen, Charles E. REGISTRATION NUMBER: 34,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORWATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
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SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
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1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
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Pred. No. 1.7e-24;
2; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: PCT/GB96/03065
PRIOR FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
ILENGTH: 51
TYPE: PRT
TYPE: PRT
PRESENT NOS SEQ ID NO SEQ
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Job time : 56 secs
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1 Similarity 92.0%;
46; Conservative
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Best Local Similarity
Matches 46; Conserva
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Pred. No. 1.7e-24;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rees, Sarah
TILLE OF INVENTION: Antifungal Proteins
FILLE REPERBNCE: 50094PPDDIV
CURRENT APPLICATION NUMBER: US/10/389,361A
CURRENT FILLING DATE: 2003-03-13
PRIOR PILLING DATE: 1998-08-07 0/7,948
PRIOR PILLING DATE: 1996-02-28
PRIOR FILLING DATE: 1996-03-28
PRIOR FILLING DATE: 1996-03-28
PRIOR PILLING DATE: 1996-03-28
PRIOR PILLING DATE: 1996-03-28
PRIOR PILLING DATE: 1996-03-28
PRIOR PILLING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 141
SCOTTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: SI
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APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
ITILE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN OJSUV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/077,951
PRIOR FILING DATE: 1998-06-10
; PRIOR FILING DATE: 1998-12-13
                                                                                                                                                                                                                                                                                                        Sequence 35, Application US/10388361A Publication No. US20030226169A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Borremain, Frans
De Samblanx, Genoveva
Sitjtema, Lolke
Meloen, Robbert
Puijk, Wouver
Schaaper, Wilhelmus
Broekeart, Willem
Van Gelder, Wilhelmus
Rees, Sarah
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                                                                Query Match 93.4%;
Best Local Similarity 92.0%;
Matches 46; Conservative
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; ORGANISM: Raphanus sativus
US-10-681-972-19
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; ORGANISM: Raphanus sativus
US-10-388-361A-35
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Best Local Similarity 92.0
Matches 46; Conservative
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US-10-006-252A-9
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 93.4%; Score 281; DB 13; Length 51; Local Similarity 92.0%; Pred. No. 1.7e-24; les 46; Conservative 2; Mismatches 2; Indels
RESULT 15
US-10-006-252A-20
Sequence 20, Application US/10006252A
PUDIcation No. US20020152498A1
GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekeart, Willem
APPLICANT: Rees, Sarah
TITLE REFERENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1996-12-13
SUFUNDER OF SEQ ID NOS: 77
SOFTWARE: PARCHING VET. 2.0
SEQ ID NOS: 77
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May 11, 2004, 16:54:24 ; Search time 20 Seconds (without alignments) 240.479 Million cell updates/sec
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301
1 KLCERSSGTWSGVCGNNNAC.....QHGSCNYVFPAHKCICYFPC 50
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                         283366 seqs, 96191526 residues
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                      Title:
Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	antifungal protein		antifungal protein	Η.	ar	4012	probable antifunga	cal p	MP1	antifungal protein	O	antifungal protein	defensin AMP1 - Cl	antifungal protein		antifungal protein	щ.	antifungal protein	defensin AMP1 - Ae		probable gamma-thi	er-sp	pitl protein (clon	t-th	nknow	gamma-zeathionin 1	gamma-purothionin	thionin precursor,
QI	T10243	T10183	T10823	117	T02622	578	0262	632	S66221	S28991	S12246	888	521	9	മ	S28994	866220	828990	866218	F96591	T14866	A.	n	857809	ø	5831	811529	2357
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Query Match Length	79	80	80	80	80	80	80	56	20	30	161	27	49	25	27	26	54	27	20	80	83	152	83	105	55	47	47	105
Query Match	100.0	93.	93.4	92.7	92.7	91.0	٥.	55.5	53.8	50.2	ω.	•	46.7	45.8	45.5	•			w.	38.7	38.7	'n.	33.7	27.4	26.7		25.1	
Score	301	oo	œ	7	7	7	7	9	9	ß	4	4	•	138	137	m	134.5	3	29.	16.	è.	05.	91.	ų.	80.5	۲.	5	
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gamma-thionin SI-a	hordothionin gamma	gamma-thionin SI-a	gene serrate prote	surface protein	neurotoxin III	neurotoxin II prec	proteinase inhibit	defensin AMP2 - Da	proteinase inhibit	disease resistance	defensin 1 precurs	transforming growt	disease resistance	purothionin gamma	neurotoxin XI -	ខ្ម
S69146	\$13849	S69144	S16148	T28669	NTSR3B	NTSR2A	D84433	S66222	T02667	T06599	JC7897	A35626	T06766	S11530	NTSREB	ALIGNMENTS
N	N	N	7	~	Н	Н	N	7	7	7	~	7	7	7	Н	
47	47	47	1408	2233	64	85	73	20	81	72	82	1394	74	47	65	
24.8	24.8	24.8	24.6	24.4	24.3	24.3	24.1	23.9	23.8	23.4	23.4	23.4	23.3	23.1	22.9	
74.5	74.5	74.5	74	73.5	73	73	72.5	72	71.5	70.5	70.5	70.5	70	69.5	69	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

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Tilling protein 1 precursor - radish Cipacies Raphanus Sativus (radish) C. Defecies Raphanus Sativus (radish) 16-Jul-1999 #sequence_revision 16-Jul-1999 #sequence_revision 16-Jul-1999 #sequence_revision 170176; A2842 C. Defection Tilling Radish Radish Research Tilling Radish Research Radish Research Radish Research Radish Research Radish 
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Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: 24-Mar-1399 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
Cispecies: D84655
Ricoursley, S.D.; Kanl, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S submitted to the EMBL Data Library, August 1998
A; Pescription: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
A; Recession: T02622
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-60 cROUS
A; Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413711
A; Experimental source cultivar Columbia
A; Experimental source cultivar Columbia
A; Experimental source cultivar Columbia
B; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.; N., Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487; PMID:10517197
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20
                                     11 KLCQRPSGTWSGVCGNNNACKNQCIRLEKARHGSCNYVFPAHKCICYFPC
1 KLCERSSGTWSGVCGNNNACKNOCIRLEGAQHGSCNYVFPAHKCICYFPC
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       30 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: T10183
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Gocule type: mRNA
A,Gocs-references: EMBL:X97318
A,Stross-references: EMBL:X97318
A,Stross-references: EMBL:X97318
A,Gocs-references: EMBL:X97318
A,Gocs-references: EMBL:X97318
A,Gocs-references: EMBL:X97318
C,Gocnetics:
A,Gocne: AFP4
C,Superfamily: gamma-thionin
C,Keywords: antifungal
F,1-29/Domain: signal sequence #status predicted <MGC>
F,30-80/Product: antifungal protein 4 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.7%; Score 282; DB 2; Length 80; Best Local Similarity 90.0%; Pred. No. 2.5e-23; Matches 45; Conservative 3; Mismatches 2; Indels
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F;1-43/Domain: signal sequence #status predicted <SIG>
F;44-80/Product: antifungal protein 2 #status predicted <MAT>
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A;Gene: AFP2
C;Function:
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Conservative
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Best Local Simi
Matches 26;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Cornary.
C;Species: Cornary.
C;Accession: F96787
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.Wing, M.R.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Restdues: preliminary
A;Residues: Ps6787
A;Status: preliminary
A;Residues: 1-80 <STO>
A;Cross-references: GB:AE005173; NID:g6721100; PIDN:AAF26754.1; GSPDB:GN00141
A;Gene: T4012.7
A;Map Position: 1
C;Superfamily: gamma-thionin
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Accession: T02621, E34655
B.Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, August 1998
A.Reference number: 214681
A.Reference: Constant of the GB/EMBL/DDBJ
A.Reference: Cross-references: EMBL:ACO04747; NID:g3413696; PID:g3413721
A.Residues: 1-80 cROD-A.Residues: cultivar Columbia
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
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A;Accession: D84655
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-80 <STO>
A;Residues: 1-80 <STO>
A;Cross-references: GB:AE002093; NID:g3413711; PIDN:AAC31234.1; GSPDB:GN00139
C;Genetics:
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Best Local Similarity 90.0
Matches 45; Conservative
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A,Introns: 22/1
C,Superfamily: gamma-thionin
                                                                                                                                                                      A;Gene: At2g26010; T19L18.18
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Appochetical protein F14Pl.6 - Arabidopsis thaliana

(Special 1970)

(Special 2070)

(Special 
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente: Nature 402, 751-768, 1999
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Actesion: E84655
A;Acteus: preliminary
A;Molecule type: DNA
A;Residues: L-80 <STO>
A;Genetics:
A;Genetics:
A;Gene: AL2g26020; T19L18.17
A;Map position: 2
A;Introns: 22/1
C;Superfamily: gamma-thionin
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N;Alternate names: seed antifungal protein
C;Species: Dahlia merckii
C;Species: Dahlia merckii
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C;Accession: S66221
R;Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Let
R;Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Let
A;FEBS Lett. 369, 257-262, 1995
A;Title: Isolation and characterisation of plant defensins from seeds of Asteraceae,
A;Reference number: S66218; MUID:95354848; PMID:7628617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.4%; Score 272; DB 2; Length 80; 88.0%; Pred. No. 2.9e-22; iive 3; Mismatches 3; Indels
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52.0%; Pred. No. 3.2e-11;
live 6; Mismatches 18,
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A; Residues: 1-50 < OSB>
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A; Reference number: S28989; MUID:93138130; PMID:8422949

A,Accession: S28989 A,Molecule type: protein A,Residues: 1-27 <TER> C,Superfamily: gamma-thionin

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Gaps

. 0

Query Match 53.8%; Score 162; DB 2; Length 50; Best Local Similarity 54.0%; Pred. No. 9.9e-11; Matches 27; Conservative 5; Mismatches 18; Indels

RESULT 11

C; Keywords: antifungal

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RESULT 14

defensin AMPI - Clitoria ternatea

MyAlternate names: seed antifungal protein

C;Species: Clitoria ternatea

R;Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Leuven, RsESS Lett. 368, 257-262, 1995

A;Ribalation and characterisation of plant defensins from seeds of Asteraceae, Fabs A;Accession: S66219

A;Accession: S66
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C;Species: Sinapis alba (white mustard)
C;Date: 228-994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
C;Accession: 528993
R;Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, FEBS Lett. 316, 233-240, 1993
A;Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae A;Reference number: 528993
A;Accession: $28993
A;Accession: $28993
A;Accession: $28993
A;Accession: $28993
A;Accession: $28993
C;Superfamily: gamma-thionin
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49.1%; Pred. No. 1.9e-08;
tive 5; Mismatches 13; Indels
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Best Local Similarity 95.8%; Pred. No. 2.1e-08;
Matches 23; Conservative 0; Mismatches 1; Indels
    Length 27;
47.2%; Score 142; DB 2; Length 27
96.0%; Pred. No. 8.2e-09;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                     56
                                                                                                                                                                                    1 KLCERSSGTWSGVCGNNNACKNOCI 25
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Best Local Similarity 49.19
Matches 26; Conservative
         Query Match
Best Local Similarity 96.0<sup>5</sup>
Matches 24; Conservative
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C;Species: Helianthus annuus (common sunflower)
C;Species: Helianthus annuus (common sunflower)
C;Date: 2:1Nov-1993 #sequence_revision 26-May-1995 #text_change 15-Sep-2003
C;Accession: S12246
R;Domon, C.; Evrard, J.L.; Herdenberger, F.; Pillay, D.T.N.; Steinmetz, A.
B;Domon, C.; Evrard, J.S.; A3-646, 1990
A;Title: Nucleotide sequence of two anther-specific cDNAs from sunflower (Helianthus ann A;Reference number: S12245; MUID:91338702; PMID:2102380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Brassica rapa (turnip)
C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
C;Accession: S28989
C;Accession: S28989
FBS Lett. 316, 233-240, 1993
A;Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae
                                                                                                                                                                                                                                                                                                                         antifungal protein 1 - rape (fragment)
C;Species: Brassica napus (rape)
C;Species: Brassica napus (rape)
C;Species: Brassica napus (rape)
C;Species: 25-F994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
C;Accession: S28991; S28992;
R;Terras, F.R.G; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, FRBS Lett. 316, 233-240, 1993
FRTLile: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae A;Reference number: S28989; MUID:93138130; PMID:8422949
A;Rolecule type: protein
A;Residues: 1-30 cTRR>
A;Accession: S28992
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A,Molecule type: mRNA
A,Residues: 1-161 < LON
A,Cross-references: EMBL:X53375; NID:g18812; PIDN:CAA37455.1; PID:g18813
F,1-8/Domain: signal sequence (fragment) #status predicted <SIG>F;9-161/Product: anther-specific protein SP18 #status predicted <NAT>
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                                                                            1 ELCEKASKTWSGNCGNTGHCDNQCKSWEGAAHGACHVRNGKHMCFCYFNC 50
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                   1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
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50.2%; Score 151; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 9.8e-10;
Matches 26; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 46.0%; Pred. No. 1.6e-08;
Matches 23; Conservative 8; Mismatches 19; Indels
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A, Residues: 1-23 <TE2>
C, Superfamily: gamma-thionin
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RESULT 13

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00940; GAMMA_THIONIN; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
Slighal fungicide; Signal; Multigene family.
SIGNAL 1 29 POTENTIAL.
CHAIN 30 CYSTEINE-RICH ANTIFUNGAL PROTEIN 3.
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
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InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knotl.
Emm, PP00304; Gamma-thionin; 1.
ProDom; PD002594; G Purcthionin; 1.
SWART; SM00505; Knotl; 1.
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50; Conserv
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O24332 raphanus sa
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beta vulgar
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                                                                                        May 11, 2004, 16:50:53 ; Search time 11 Seconds (without alignments) 236.683 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 2000000000
                                                                                                                                                         US-10-006-252A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                          SwissProt_42:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46
64
64
64
85
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80
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161
27
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47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                              OM protein
                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                Searched:
                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
No.
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.. 0

Gaps

·, 20

Length 79; Indels

100.0%; Score 301; DB 1; 100.0%; Pred. No. 5.4e-27;

0; Mismatches

Conservative

3B5289FCFEA48936 CRC64;

BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

29 79 64 73 75 8555 MW;

1 30 32 43 49 53 79 AA;

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homo sapien
homo sapien
pisum sativ
triticum ae
                                                                                              leiurus qui
brachydanio
          pisum sativ
                                                               buthus occi
hirudo medi
                                                                                     rattus norv
                                                                                                                     vigna ungui
                                                                                                                                                                                                                                                                                   Brassica napus (Rape).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Nachan;
Sobn U., Lee C.M., Lee M.H., Kim U.H.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
cations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
         000178
00178
00178
001736
001736
001789
001789
000789
000789
000789
                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 3 precursor (AFP3).
                                                                                                                                                                                                           79 AA
                                                                                                                                                     ALIGNMENTS
                                                                                             SCX5_LEIQU
JAG3_BRARE
THGC_VIGUN
PSD2 PEA
D230 PEA
LTBS HUMAN
LTBL HUMAN
DR39 PEA
THG2 WHEAT
SCXB BUTOC
ITHC HIRME
S213 RAT
 SEQUENCE FROM N.A.
 AFP3 BRANA
Q39313;
70.5
70.5
70.5
70.5
69.5
68
68
68
68
68
68
68
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77.74.70

TI MON TI

70.180

07C7=000=01=81

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
                                                                                          STRAIN-CV. Ronde Rode Kleine Witpunt; TISSUE-Seed;
STRAIN-CV. Ronde Rode Kleine Witpunt; TISSUE-Seed;
Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
Broekaert W.F.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic cations (By similarity).
-!- FUNCTLUIAR LOCATION: Secreted.
-!- SUBCELLUIAR Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 KLCERSSGTWSGVCGNNNACKNQCINLEGARHGSCNYIFPYHRCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SMO505; Knotl; 1.
PROSITE; PS00940; GAMMA THONIN; 1.
Plant defense; Pungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X97318; CAA65983.1; -.
PIR, T10183; T10183.
HSSP; P30231; 1AVJ.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Xnot1.
Pfam; PP00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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SEQUENCE
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on the use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                         Raphanus sativus (Radish).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Raphanus.
NCBI_TaxID=3726;
                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probom; PD00255", -1.
SWART; SM00505; Knotl; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family.
Plant defense; Cungicide; Signal; Multigene family.

POTENTIAL.

CYSTEINE-RICH ANTIFUNGAL PROTEIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 301; DB 1; Length 79; 100.0%; Pred. No. 5.4e-27; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                [1] SEQUENCE FROM N.A. STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed; Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BAFA80465DB48548 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          cations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-FBB-2003 (Rel. 41, Last amnotation update)
Cysteine-rich antifungal protein 3 precursor (AFP3).
                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P30231, 1AYJ.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knotl.
Pfan; PP00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
79
79
64
73
75
8479 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X97319; CAA65984.1; -.
                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, T10243; T10243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1
30
32
43
49
53
79 AA;
                                                                                                    AFP3 RAPSA
024332;
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DISULFID
DISULFID
SEQUENCE
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Best Local 8
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RAPSA
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STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
MEDLINE=9529355; PubMed=7780308;
Terrae F.R.G., Eggermont K., Kovaleva V., Raikhel N.V., Osborn R.W.,
Kester A., Rees S.B., Torrekens S., van Leuven F., Vanderleyden J.,
                                                                                                                                         Raphanus sativus (Radish).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Esassicales; Brassicaceae; Raphanus.
                                                  01-APR-1993 (Rel. 25, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 2 precursor (AFP2).
                  80 AA
                  PRT;
                  STANDARD;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                    RAPSA
AFP2_RAPSA
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Gaps

·, 20

50; Conservative

Similarity

Best Loca Matches

30 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 79 1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC

В

Cysteine-rich antifungal protein 4 precursor (AFP4).

Raphanus sativus (Radish)

16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)

AFP4 RAPSA
ID AFP4 RAPSA
ID AFP4 RAPSA
DT 16-0CT
DT 16-0CT
DT 28-FEB
DE CYSTEI
GN AFP4.

80 AA

PRT;

STANDARD;

AFP4 RAPSA 024331;

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Gaps

.. 50

Score 282; DB 1; Length 80; Pred. No. 6.9e-25; A Mismatches 2; Indels

93.78; 8873 MW;

CXSTEINE-RICH ANTIFUNGAL PRC PYRROLIDONE CARBOXYLIC ACID SIMILARITY).

30

POTENTIAL

BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

80 65 74 76

33 44 50 54 80 AA;

us-10-006-252a-10.rsp

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                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 34, Last sequence update)
01-07-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 1 (APP1) (M1)
Sinapis alba (White mustard) (Brassica hirta).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Sinapis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
       "Small cysteine-rich antifungal proteins from radish: their role in host defense.";
Plant Cell 7:573-588(1995).
                                                                                        Terras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F., Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.; "Analysis of two novel classes of plant antifungal proteins from radish (Raphanus sativus L.) Seeds."; J. Biol. Chem. 267:153109(1992).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ςį
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 KLCQRPSGTWSGVCGNNNACKNQCIRLEKARHGSCNYVFPAHKCICYFPC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYSTEINE-RICH ANTIFUNGAL PROTEIN PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                     -!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      746110D9A8CE6370 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00940; GAMMA THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 281; DB 1;
Pred. No. 8.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                    EMBL; U18556; AAA69540.1; -...
HSSP; P30231; T10823.
INCEPTO; P30231; LAVU.
INCEPTO; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
ProDom; P0002594; Gamma-thionin, 1.
ProDom; P0002594; G Purchionin; 1.
SWART; SM00505; Knot1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Seed;
MEDLINE=96433791; PubMed=8836771;
Neumann G.M., Condron R., Polya G.M.,
                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted
                                                                                MEDLINE=92348373; PubMed=163977;
Cammue B.P.A., Broekaert W.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8875 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Conservative
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80
80
80
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                                                        SEQUENCE OF 30-65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 AA;
                                                                                                                                                                cations
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AFP1_SINAL
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MEDILINE=98300344; PubMed=9636715;
Fant F., Vranken W.F., Broekaert W.F., Borremans F.A.M.;
"Determination of the three-dimensional solution structure of Raphanus
sativus antifungal protein 1 by 1H NVR.";
J. Mol. B101. 279:257-270(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=R.sativus; STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed; MEDLINE=95299350; PubMed=7780308; Terras F.R.G., Eggermont K., Kovaleva V., Raikhel N.V., Osborn R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Ruphanus sativus (Radish).
Bukarus viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicoryledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00505; Knotl; 1.

PROSITE; PS00940; GAMMA_THIONIN; 1.

Plant defense; Fungicide; 3D-structure; Pyrrolidone carboxylic acid.

MOD RES

DISULFID

4 51

FYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                       Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W., anderleyden J., Cammue B.P.A., Broekaert W.F.; "A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae species."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Forms oligomers in its native state.
-!- MASS SPECTROMETRY: MW=5677; MW ERR=1.0; METHOD=Electrospray.
"Purification and mass spectrometry-based sequencing of yellow mustard (Sinapis alba L.) 6 kDa proteins. Identification as antifungal proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KLCERPSGTWSGVCGNNNACKNQCINLEKARHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 279; DB 1; Length 51;
Pred. No. 9.8e-25;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the plant defensin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFP1_BRANA STANDARD; PRT; 80 AA.
P30225; Q41163;
10-AR-1993 (Rel. 25, Created)
16-CT-2001 (Rel. 40, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 1 precursor (AFP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   770990E72DD1C469 CRC64;
                                                                                          int. J. Pept. Protein Res. 47:437-446(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB; 1AYJ; 28-JAN-98.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
                                                                                                                                                                                                                  MEDLINE=93138130; PubMed=8422949;
                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 316:233-240(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.7%;
92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5695 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 92.0
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3708, 3726;
                                                                    antifungal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 AA;
                                                                                                                                                      SEQUENCE OF 1-25.
                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR.
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SEQUENCE
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                                                                                                                                                           SEQUENCE OF 30-73.
SPECITS-B. nague; TISSUE=Seed;
MEDLINE=93138130; PubMed=8422949;
Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
Brassicaceae species.;
FEBS Lett. 316:233-240(1993).
Kester A., Rees S.B., Torrekens S., Van Leuven F., Vanderleyden J., Cammue B.P.A., Broekaert W.F., "Small cysteine-rich antifungal proteins from radish: their role in host defense.";
                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-R. Sativus; IISSUE-Seed; MEDLINE-92348373; PubMed-163977; Terras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F., Terras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F., Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.; "Analysis of two novel classes of plant antifungal proteins from J. Seeds."; Seeds."; Seeds."; J. Bacal. Chem. 257:15310-15309(1992).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYSTEINE-RICH ANTIFUNGAL PROTEIN 1.
PYRROLIDDONE CARBOXYLIC ACID.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
05B90FAAC8DA6C2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTITE, PROMOBOUR THIONIN, 1.
PROSTITE, PROMOBOUR CARMARA THIONIN, 1.
Plant defense, Fungicide, Signal, Multigene family,
Pyrrolidone carboxylic acid.
29 CYSTEINB-RICH ANTIFUNGAL E
SIGNAL 1 29 CYSTEINB-RICH ANTIFUNGAL E
MOD RES 30 30 PYRROLIDONE CARBOXYLIC ACID
DISULFID 33 80 BY SIMILARITY.
DISULFID 54 65 BY SIMILARITY.
DISULFID 54 65 BY SIMILARITY.
DISULFID 54 76 BY SIMILARITY.
SEQUENCE 80 AA, 8734 MW, 05B90FAACGDAGC2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Forms oligomers in its native state.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P30231; 1AVJ.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G Purothionin; 1.
SWART; SM00505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U18557; AAA69541.1; -. PIR; T10176; T10176.
                                                                                                             Plant Cell 7:568-573(1995).
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 30-73.
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             SOURCE STATE STATE
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Nature 402:761-768(1999).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic cations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: Belongs to the plant defensin family.

"Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";

MEDLINE-20083487; PubMed=10617197;

MEDLINE-20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,

Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Unayam L.,

Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Craesy T.H.,

Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,

Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,

nimaruoppis cuaitama (mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis. Probable cysteine-rich antifungal protein At2g26010 precursor (AFP). AT2G26010 OR T19L18.18. Arabidopsis thaliana (Mouse-ear cress).

SEQUENCE FROM N.A. eurosids II; Bra NCBI TaxID=3702;

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ilarity 90.0%;
Conservative
             Best Local Similarity
Matches 45; Conser
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                                                                              KLCERPSGTWSGVCGNNNACKNQCINLEKARHGSCNYVFPAHKCICYFPC
                                                          1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
Score 279; DB 1; Length 80; Pred. No. 1.5e-24;
                              3; Indels
                                                                                                                                                                                          (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                80 AA
                                1; Mismatches
                                                                                                                                                               PRT;
 92.7%;
               Local Similarity 92.0
nes 46; Conservative
                                                                                                                                                                STANDARD;
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16-OCT-2001 (
28-FEB-2003 (
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ARATH

AFP2 AR7 080995;

Query Match

Best Loca Matches

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20
                                                                                                                                              31 KICEKPSGTWSGVCGNSNACKNQCINLEGAKHGSCNYVFPAHKCICYFPC 80
                                                                                                                1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
Score 279; DB 1; Length 80; Pred. No. 1.5e-24; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                       AFP1 ARATH

ID AFP1 ARATH
STANDARD; PRT; 80 AA.

AC P302Z4; Q42179;
DT 01-APP-137 [Rel. 25, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 28-FEB-2003 [Rel. 41, Last annotation update)
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Gaps

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CYSTEINE-RICH ANTIFUNGAL PROTEIN

PROBABLE

80 30

30

MOD_RES

SMART; SM00505; KnoFl, 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family;
Plant defense; encoxylic acid.
1 29 BY SIMILARITY.

HSSP, P30231, 1AYJ. InterPro, IPR008176, Gamma-thionin. InterPro, IPR003614, Knotl.

EMBL; AC004747; AAC31234.1; -. PIR; T02622; T02622.

ProDom; PD002594; G_Purothionin; 1. Pfam; PF00304; Gamma-thionin; 1.

PYRROLIDONE CARBOXYLIC ACID (BY

SIMILARITY)

BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
99EIBOD4443AD67B CRC64;

33 44 50 54 80 AA;

DISULFID DISULFID DISULFID DISULFID SEQUENCE Query Match

92.7%;

Fri May 14 09:47:39 2004

RY SUCURNE FOUR NA.

RY SUCURNE FOUR NA.

RY SUCURNE FOUR NA.

RY SUCURNE FOUR NA.

RY SUCURNE FOUR SOLUTION STATE C. STRAIN S. THOOLOGIS A., ECKET J.R., Palm C.J., Pedman C.L., Brooks S.Y.,

RY Minte O., Alonso J., Aladi H., Araujo R., Bowman C.L., Brooks S.Y.,

RY Suching M.K., Conn L., Conway A.B., Chenk R.F., Chin C.W.,

RY Ching M.K., Conn L., Conway A.B., Cheng J.-D., Fong B., Fulia C.Y.,

RY Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Huizar L.,

RY Hunter J.L., Jonkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RY Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Leiz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Liu Z.A., Luros J.S., Malti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.N.;

RY Sun D., Yu G., Fraser C.M., Venter J.C., Davis R.N.;

"Saguence and analysis of chromosome I of the plant Arabidopsis This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch) protein S18 homolog).
AFPI OR PDF1.1 OR ATIG75830 OR T4012.6 OR T4012.7.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis. Cysteine-rich antifungal protein 1 precursor (AFP1) (Anther-specific Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W., Vanderleyden J., Cammue B.P.A., Broekaert W.F.; Anney family of basic cysteine-rich plant antifungal proteins from Brassicaceae species. "FESS Lett. 316:233-240(1993).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases. MEDIINE=99178804; PubMed=10080719;
Williams R.W., Clark S.E., Meyerowitz E.M.;
Genetic and physical characterization of a region of Arabidopsis chromosome 1 containing the CLAVATA1 gene.";
Plant Mol. Biol. 39:171-176(1999). Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases. -!- SUBUNIT: Forms oligomers in its native state. -!- SUBCELLULAR LOCATION: Secreted. -!- SIMILARITY: Belongs to the plant defensin family. SEQUENCE FROM N.A. STRAIN=Cv. Columbia; TISSUE=Seed; MEDLINE=93138130; PubMed=8422949;

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Gaps
                                                                                                                                                                      CYSTEINE-RICH ANTIFUNGAL PROTEIN 1. PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                Score 274; DB 1; Length 80;
Pred. No. 5.3e-24;
2; Mismatches 3; Indels
                                                                                                                                                                               PYROLIDONE CARBOXYLIC AC.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
C -> F (IN REF. 1).
99F34ABDA360441F CRC64;
                                                                                             ProDom, PD002594; G-Purothionin; 1.
MART: SM0505, Knotl; 1.
PROSITE, PS00940; GAMMA_THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                           2; Mismatches
          EMBL; AF049870; AAD02502.1; --
BMBL; AC007296; AAF26754.1; --
PIX; F96787; F96787.
HSSP; P30231; 1AYJ.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR008176; Knot1.
Pfam; PF00304; Gamma-thionin; 1.
                                                                                                                                                                     80
30
80
65
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74
33
8709 MW;
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DISULFID
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01-APR-1993 (Rel. 25, Created)
01-OTT-1996 (Rel. 34, Last sequence update)
08-FEB-2003 (Rel. 41, Last amoretaion update)
Cysteine-rich antifungal protein 2A (AFP2A) (M2A)
Sinapis alba (White mustard) (Brassica hirta) 51 AA PRT; STANDARD; AF2A SINAL T 9 SINAL

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacee; Sinapis.

MEDLINE=56433791, PubMed=8836771; Neumann G.M., Condron R., Polya G.M., "Purification and mass spectrometry-based sequencing of yellow mustard (Sinapis alba L.) 6 kDa proteins. Identification as rissum=seed; SEQUENCE

Pept. Protein Res. 47:437-446(1996). antifungal proteins."; SEQUENCE OF 1-26.

rissum=seed;

Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W., Vanderleyden J., Cammue B.P.A., Broekaert W.F.; A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae species.", FEBS Lett. 316:233-240(1993). MEDLINE=93138130; PubMed=8422949;

cations.
--- SUBUNIT: Forms oligomers in its native state.
--- MASS SPECTROMETRY: MW=5705; MW ERR=0.8; METHOD=Electrospray.
--- SIMILARITY: Belongs to the plant defensin family.

HSSP, P30231; 1AYJ. InterPro; IPR008176; Gamma-thionin. InterPro; IPR003614; Knot1. Pfam; PF00304; Gamma-thionin; 1. ProDom; PD002594; G_Purothionin; 1.

EMBL; Z27258; CAA81770.1; -. EMBL; Z29957; CAA82845.1; -.

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                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 41, Last annotation update)
Probable cysteine-rich antifungal protein At2g26020 precursor (AFP).
AT2G26020 OR T19I18.17.
AT2G26020 OR T19I18.17.
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; rosids; eurosids: II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV. Columbia, MEDLINE=20083497; PubMed=10617197; Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Bujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.D., Buell C.R., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman M.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Possesses antifungal activity sensitive to inorganic cations (By similarity).
SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                    1 KLCERSSGIWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
                                                                                                                                                                                                                                                                                                                                                         2 KLCQRPSGTWSGVCGNNNACRNQCINLEKARHGSCNYVFPAHKCICYFPC 51
R SMART; SM00505; Knotl; 1.

R PROSITE; PS00940; GAWA, THIONIN; 1.

R PROSITE; PS00940; GAWA, THIONIN; 1.

R PUBLICATION CARBOXYLIC ACID.

PT MOD_RES 8 8 PHOSPHOSTLATION (BY CDPK).

FT MOD_RES 8 8 PHOSPHOSTLATION (BY CDPK).

FT DISULPID 4 51 BY SIMILARITY.

FT DISULPID 15 36 BY SIMILARITY.

FT DISULPID 21 45 BY SIMILARITY.

TSULFID 25 MW; 1C7F50E72DC945BI CRC64;
                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the plant defensin family.
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Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                        Score 273; DB 1;
Pred. No. 4.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 AA.
                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AC004747; AAC31244.1; -.
PIR; T05621; T02651.
BSSP; P30231; LAY.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00304; Gamma-thionin; 1.
                                                                                                                                                                                                                                        90.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                   44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFP3_ARATH
080994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thaliana."
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                 PROBABLE CYSTEINE-RICH ANTIFUNGAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. PROBABLE CYSTEINE-RICH ANTIFUNGAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. Columbia, MBDLINE-99397451; PubMed=10470850; Raneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H., Kaneko T., Tabata S.; Structural analysis of Arabidopsis thaliana chromosome S. IX. Sequence features of the regions of 1,011,550 bp covered by seventeen pl and TAC colons."
                                                                                                                                                                                                                                                                                                                                            APP4 ARATH STANDARD; PRT; 80 AA.

Q9FIZ3; P82786;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cysteine-rich antifungal protein LCR77 precursor (AFP).
LCR77 OR ATGS4420 OR MFC16-8.
LCR77 OR ATGS4420 OR MFC16-8.
Exabidopsis thaliana (Mouse-ear cress).
Exharyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NIBI_TAXID=3702;
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vanoosthuyse V., Miege C., Dumas C., Cock J.M.;
Submitted (JUN-2000) to Swiss-Prot.
-!- FUNCIION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                           .,
                                                                                                                                                                                                                                                               31 KLCEKPSGTWSGVCGNSNACKNQCINLEGAKHGSCNYVFPAHKCICYVPC 80
                                                                                                                                                                                                                                            1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
                                             PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                             Length 80;
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                                                            SIMILARITY).
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-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: Belongs to the plant defensin family.
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Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
SIGNAL
1 29 POTENTIAL.
CHAIN 30 80 PROBABLE CYSTEINE-RICH
                                                                                                                                                                          Score 272; DB 1;
Pred. No. 8.8e-24;
BY SIMILARITY
                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IRR008176; Gamma-thionin.
InterPro: IRR003614; Knotl.
Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB017065; BAB09149.1; -. HSSP; P30231; 1AYJ.
                                                                                                                                                                            90.4%;
                                                                                                                                            8640 MW;
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                                                                                                                                                                                                              Conservative
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Best Local Similarity
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80 AA;
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AC P30227;
DT 01-APR-1993
DT 01-FEB-1994
DT 28-FEB-2003
DE Cysteine-ric
OS Brassica rap
OC Bukaryota; V
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DISULFID
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 2B (ARP2B) (M2B).
Simapis alba (White mustard) (Brassica hirra).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; NCTL TAXID=3728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Int. J. Pept. Protein Res. 47.437-446(1996).
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                               1- SUBUNIT: Forms oligomers in its native state.
1- MASS SPECTROMETRY: MW-5840; MW ERR=1.2; METHOD=Electrospray.
1- SIMILARITY: Belongs to the plant defensin family.
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       PYRROLLDONE CARBOXYLIC ACID (BY SIMILARITY).
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                                                                                                                1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
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Neumann G.M., Condron R., Polya G.M.;
"Purification and mass spectrometry-based sequencing of yellow
mustard (Sinapis alba L.) 6 kDa proteins. Identification as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLCERSSGTW-SGVCGNNNACKNOCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 211.5; DB 1; Length 52;
Pred. No. 2.9e-17;
6; Mismatches 8; Indels
                                                                                  Length 80;
                                                                       Score 272; DB 1,
"red. No. 8.8e-24;
"red 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A060FCBC13A8D1FB CRC64;
                                                                                                                                                                                 52 AA
                                                                                                 3; Mismatches
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InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knorl.
Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G Purchionin; 1.
SWART; SM00505; Knorl; 1.
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5856 MW;
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                                                                                       Local Similarity 88.0
hes 44; Conservative
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Matches 36; Conservative
                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                             antifungal proteins.";
                                                             80 AA;
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P22357;
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Q10989;
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AF2B_SINAL
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AC P22357
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

SEQUENCE TROM N.A.

Model STAIN-cv. HA401B / Cargill; TISSUE-Anther;

M Domon C., Evrard J.-L., Herdenberger F., Pillay D.T.N., Steinmetz A.;

R (Helianthus annua L.)..;

R (Helianthus annua L.)..;

Plant Mol. Biol. 15:643-646 (1990).

C -!- FUNCTION: Anther-specific cell wall protein which could contribute contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                  eudicots; asterids;
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01-AUG-1991 (Rel. 19, Created)
01-AUG-1999 (Rel. 19, Last sequence update)
01-AUG-1994 (Rel. 29, Last amnostation update)
Anther-specific protein SP18 precursor (Fragment).
Helianthus annuus (Common sunflower).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnolliophyta, eudicotyledons, core eudicots, asteriarganulids; Asterales, Asteraceae, Asteroideae, Heliantheae,
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 21, Last sequence update)
Cysteine-rich antifungal protein 1 (AFP1) (Fragment).
Brassica rapa (Turnip).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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PROLINE DOMAIN.
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HSSP; P30231; 1AVJ.
InterPro; 1PR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
Pfam; PF00304; Gamma-thionin; 1.
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SWART; SM0505; KnoT; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
SIGNAL; Cell wall.
SIGNAL <1 8
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W. Vanderleyden J., Cammue B.P.A., Broekeart W.F.;

The new family of basic cysteine-rich plant antifungal proteins from Brassicaceae species.';

E. FEBS. Lett. 316:233-240(1993).

- I- FEBS. Lett. 316:233-240(1993).

- I- FUNCTION: Possesses some antifungal activity sensitive to inorganic cations and antibacterial activity against B.megaterium.

- I- SUMINIT: Perms oligomers in its native state.

- I- SIMILARITY: Belongs to the plant defensin family.

PIR; 528990; 528990.

PRSP: PS2391, 1ANJ.

RICHERPOO, IPRO08176; Gamma-thionin.

Probom, PD002594; G_Purothionin; 1.

PROSTIE; PS00940; GAMMA THIONIN; 1.

PROSTIE; PS00940; GAMMA THIONIN; 1.

PROSTIE; PS00940; GAMMA THIONIN; 1.

POD_RES.

I PERROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps,
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=51350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Varidiplantae, Streptophyta; edicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                  TISSUE=Seed,
MEDLINE=91138130; PubMed=8422949;
MEDLINE=913138130; PubMed=8422949;
Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
"A new family of basic cysteine-rich plant antifungal proteins from Passicaceae species.";
PEBS Lett. 316:233-240(1993).
-:- FUNCTION: Possesses antifungal activity sensitive to inorganic
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47.2%; Score 142; DB 1; Length 27
Best Local Similarity 96.0%; Pred. No. 7.6e-10;
Matches 24; Conservative 0; Mismatches 1; Indels
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01-FEB-1994 (Rel. 28, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich annifungal protein 2 (AFP2) (Fragment).
Brassica rapa (Turnip).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 AA; 2925 MW; 4C85BD9C611D4A9E CRC64;
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27 AA; 2891 MW; 571E6D9C611D4A9E CRC64;
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MEDLINE=93138130; PubMed=8422949;
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      Query Match
      44.5%; Score 134; DB 1; Length 27;

      Best Local Similarity 92.3%; Pred. No. 5.8e-09;

      Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

      Qy
      | KLCERSSGTWSGVCGNNNACKNOCIR 26

      Db
      2 KLCERPSGTXSGVCGNNNACKNOCIR 27

      Search completed: May 11, 2004, 16:57:18

      Job time: 39 secs
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May 11, 2004, 16:53:44; Search time 39 Seconds (without alignments) 404.511 Million cell updates/sec
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301
1 KLGERSSGTWSGVCGNNNAC.....QHGSCNYVFPAHKCICYFPC 50
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1017041 seqs, 315518202 residues
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Q94in7 brassica ol	Q8h6k0 brassica ra	Q9fs38 eutrema was	Q9fi22 arabidopsis	Q9fwr6 arabidopsis	Q8vzq7 arabidopsis	Q81sm8 helianthus	Q84zx5 artemisia v	Q9fz31 arabidopsis	Q40779 picea abies	Q8gtl2 picea abies	Q40539 nicotiana t	P82788 arabidopsis	P82789 arabidopsis	Q40128 lycopersico	Q948t2 pyrus pyrif
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	do (Cuery	March	94.4	94.0	92.7	90.4	55.5	55.5	51.2	42.9	38.7	38.7	38.4	33.7	28.7	27.7	27.4	27.1
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Gaps

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Score 284; DB 10; Length 80; Pred. No. 1e-29; 2; Indels

Query Match
Best Local Similarity 94.0%;
Matches 47; Conservative

31 KLCERPSGTWSGVCGNNNACKNQCIRLEKARHGSCNYVFPAHKCICYFPC 80 1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC

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Q948t3 pyrus pyrif Q948t4 pyrus pyrif Q94105 nicotiana e Q92410 arabidopsis Q81eg6 arabidopsis Q81eg6 arabidopsis Q81eg6 arabidopsis Q81eg6 arabidopsis Q81eg6 arabidopsis Q84t0 micotiana a Q844t0 petunia hyb Q8t2p0 lytechinus Q9t6Q0 petunia hyb Q8t2p0 lytechinus Q9t6Q0 petunia hyb Q8t2p0 lytechinus Q9t6G0 drosophila Q9t8G0 drosophila Q9t9G5 drosophila Q9t9G5 drosophila Q9t711 paramectum Q9tx03 arabidopsis Q8t205 oryza sativ Q8t205 oryza sativ Q9t766 elaeis guin Q9t766 piegeguin Q9t766 elaeis guin Q9t843 vigna radia Q8t436 vigna radia Q8t436 vigna radia Q8t436 vigna radia Q8t436 vigna radia	"IGNMENTS "IGNMENTS "IGNMENTS "I 80 AA. "I 80 AA. "I 80 BA. "I sequence update) "I annotation update) "I incotyledons; core eudicots; rosids; "I cocae; Erassica. "I censin.";
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йди грорио — попородинатия	ALIGNMENTS RT; 80 ated) t sequence t annotati tophyta; E udicotyled icaceae; B defensin. L/GenBank/ ity protei nin. ; 1. ; 1. ; 1.
0948T3 0948T4 094247 09C34105 09C347 08LEGG 08CLEGG 08CLEG 08CLEG 08T4P0 09T4P0 09T4P0 09T4P0 09T4P0 09T85 0	PRT; 80 AA. Created) Last sequence upda Last annotation up rer) reptophyta; Embryc t; eudicotyledons; t; eu
	19, 25, 25, 25, 19, 10, 11, 11, 11, 11, 11, 11, 11, 11, 11
201 105 105 105 105 105 105 105 105 105 1	PRELIMINARY; (TrEMBLrel. 19, (TrEMBLrel. 26, CUTSOr. racea (Cauliflo iridiplantae; Sa, Magnoliophyt Brassicales; Erassicales; Erassic
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 94IN7; 94IN7; 94IN7; 94IN7; 94IN7; 1-DEC-2001 1-OCT-2003 sfensin pressor ole rassica ole permatophyt ICOIL AND 3110 OCOIN PRO 00037 ABL; AJ3110 ABL; AJ3110 AGCOSTE; PRO 00037 AGCOSTE; PRO 000
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92.7%; Score 279; DB 10;
88.0%; Pred. No. 4.6e-29;
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Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                          Created)
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                                            Conservative
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Best Local Similarity
Matches 44; Conserv
                        Similarity
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01-MAR-2001
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01-OCT-2003
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01-MAR-2001
                                         44;
      Query Match
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Matches 4
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Q9FWR6
ID Q9FWF
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TISSUE=Leaf, and Stem;
MEDLINE=21011227; PubMed=11204773;
Saitoh H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;
Saitoh H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;
Production of antimiorobial defensin in Nicotiana benthamiana with a potato virus X vector.";
Mol. Plant Microbe Interact. 14:111-115(2001).
EMBL; AB012871; BAB19054.1; -.
HSSP; P30231; IAVJ.
GO; GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR00314; Knotl.
InterPro; IPR003614; Knotl.
Pfam; PF00304; Gamma-thionin.
Pfam; PF00304; Gamma-thionin.
                                                                                                                                                                Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage). Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                           Ryang S.-H., Chung S.-Y., Park Y.-S., Cho T.-J.,

"Characterization of Chinese cabbage genes induced by Pseudomonas syringae pv. tomato.";

Syringae pv. tomato.";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF528180; AAN23105.1;

EMBL, AF528180; AAN23105.1;

InterPro; IPR00176; Gamma-thionin.

InterPro; IPR00364; Knot1.

Ppfam, PF00304; Gamma-thionin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 283; DB 10; Length 80;
Pred. No. 1.4e-29;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00505; Knocl; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
SEQUENCE 80 AA; 8864 MW; 485CC5A95905E92C CRC64;
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POTENTIAL.
CF2F10ADD38FC87A CRC64;
                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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92.0%; Pred. No. ...
2; Mismatches
                                                80 AA.
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PROSITE; PS00940; GAMMA_THIONIN; 1.
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SMART; SM00505; Knotl; 1.
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Best Local Similarity 92.0°
Matches 46; Conservative
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SIGNAL
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BNA Res. 6.183-195(1999).

BNA Res. 6.183-195(1999).

BNA ROS 19000393; Fridefense/immunity protein activity; IEA.

BY THEAPPO; IPRO03614; Gamma-thionin.

R Fam., PRO0364; Gamma-thionin.

PRODOM; PRO02594; G Purothionin; 1.

PRODOM; PRO02594; G Purothionin; 1.

PRODOM; PRO02594; G Purothionin; 1.

PRODOM; PRO0459; RACE!: 1.

SR SRQUENCE 80 AA; 8550 WW; 44EIFEDB452AC76E CRC64;
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta: Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales, Brassicaceae; Arabidopsis.
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Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A.,
Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
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                                                                                                                                                                        31 KLCEKSSGTWSGVCGNNNACKNQCINLEGARHGSCNYIFPYHRCICYFPC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                   1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
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                                                                 2; Indels
Length
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -MAR-2001 (TrEMBLrel. 16, Last sequence update)
                                                                     4; Mismatches
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Pfam; PF00304; Gamma-thionin; 1.
SMART; SM00505; Knot1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helianthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                Defensin.
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                                                                                                                                                                                                             RESULT 7
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Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
Iee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Chenk R.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Rawai J., Kim C., Koesema E., Lam B., Lih J., Meyers M.C., Miranda M.,
Narusaka M., Nguyen M., Palm C.J., Sakurai T., Sacou M., Seki M.,
Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
"Pull Length CDNA of gene Atlg19610 (G1:15223595).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodeze C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
          Shinn P.,
Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RICERRSKTWTGFCGNTRGCDSQCKRWERASHGACHAQFPGFACFCYFNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query March 55.5%; Score 167; DB 10; Length 78; Best Local Similarity 52.0%; Pred. No. 2.2e-14; Matches 26; Conservative 6; Mismatches 18; Indels
                                                                                                                                                                                                   GO, GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY063933; AAL186299.1; -.
EMBL; AX164038; AAM186299.1; -.
INTERPL; AX114038; AAM45086.1; -.
INTERPTO; IPRO08176; Gamma-thionin.
Promy: PPRO0304; Gamma-thionin; 1.
PRO0315; PS00940; Gamma-mathionin; 1.
                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00505; Knočl; 1.
PROSITE; PS00940; GAMMA THIONIN; 1.
SEQUENCE 56 AA; 6403 MW; 3BD56EAA25EBC442 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS00940; GĀMMA THIONIN; 1.
SEQUENCE 78 AA; 8840 MW; A5B5DD28303A6545 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBirel. 20, Created)
U-MAR-2002 (TrEMBirel. 20, Last sequence update)
01-0CT-2003 (TrEMBirel. 25, Last annotation update)
Putative defensin AMPI protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 167; DB 10;
Pred. No. 1.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                         ProDom; PD002594; G_Purothionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                      Pfam; PF00304; Gamma-thionin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.5%;
                                                                                                   EMBL; AC024609; AAF98402.1;
PIR; G86328; G86328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 26; Conserv
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0.1-UNA'2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-UTN-2003 (TrEMBLrel. 25, Last annotation update)
Major pollen allergen Art v 1 precursor.
Artemisia vulgaris (Mugwort).
Bukaryora; Viridiplancae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Asteroideae; Anthemideae;
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Himly M., Jahn-Schmid B., Dedic A., Kelemen P., Wopfner N., Altmann F., van Ree R., Briza P., Richter K., Ebner C., Ferreira F.; "Art v. 1, the major allergen of mugwort pollen, is a modular glycoprotein with a defensin-like and a hydroxyproline-rich domain."; FASEB J. 17:106-108(2003).

EMBL, AF493943, AAO34900.1; -
GO; GO:0003793; Fidefense/immunity protein activity; IEA.

InterPro; IPR008164; Knot1.

InterPro; IPR008614; Knot1.
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Lu G.;
1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 108;
                              1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF364865, AAM77914.1;
GO, GO:0003793, F:defense/immunity protein activity, IEA.
InterPro; IPR008176; Gamma-thionin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G Purothionin; 1.
SMART; SM0505; KnoEl; 1.
SEQUENCE 108 AA; 11866 MW; 631ECD8F02F21AD0 CRC64;
                                                                                                                                                                                                                                                   01-0cT-2002 (TrEMBLrel. 22, Created)
01-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Oxalate oxidase confers Sclerotinia resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 154; DB 10;
Pred. No. 1.5e-12;
6; Mismatches 19;
                                                                                                                                                                                                  108
                                                                                                                                                                                                                                                                                                                                                                          Helianthus annuus (Common sunflower)
                                                                                                                                                                                                  PRT;
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MEDLINE=22409970; PubMed=12475905;
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DB 10;

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Query Match
Best Local Similarity
Matches 20; Conserv
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WHOLINE=21016719; PubMed=11130712;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
Theologis A., Ecker J.R., Palm C.J., Bowman C.L., Brooks S.Y.,
Theologis A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
The Chung M.K., Conn L., Conway A.B., Fong B., Fujii C.Y.,
Chung M.K., Conn L., Conway A.B., Hansen N.F., Hughes B., Huizar L.,
The Coldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
Chung M.K., Conn L., Gondsmith A.D., Lenz C.A., Li J.H., Li Y.-P.,
Thin C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Li Y.-P.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maitis R., Marziali A.,
Milischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
Bai G., Peterson J., Pham P.K., Riazo M., Rooney T., Rowley D.,
Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
A. Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
M. U., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                            1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHK-----CICYFPC 50
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SEGUENCE FROM N.A.

Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,

Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A.,

Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,

Howng B., Ju A., Liu S., Mukharsky, N., Pham P., Sakano H., Shinn P.,

Torium, M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                14;
                                                                                                                                                                                                                                                                                       01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative antifungal protein (Cysteine-rich antifungal protein,
                                                                              Length 132;
                  POTENTIAL.
MAJOR POLLEN ALLERGEN ART V 1.
745249C89919F316 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSE, P30231; 1AVJ.
GO, G0.0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 AA; 9139 MW; BEFBF4ACA7974071 CRC64;
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1 Similarity 45.6%; Pred. No. 3.6e-09;
26; Conservative 6; Mismatches 11:
                                                                                                                                                                                                                                                           80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AC064840; AGG00880.1; -... EMBL; AC069144; AAG51104.1; -... PIR; F96591; F96591.
                    1 24 PC
25 132 MJ
132 AA; 13404 MW;
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                      r24C10.12 OR F14C21.57.
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                                                                                  Query Match
Best Local
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                                                                                                  Best Loc
Matches
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                                                                                               Gaps
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TISSUE=Root;
Sharma P., Linneborg A.;
Sharma P., Linneborg A.;
Isolation and characterization of a cDNA encoding a gamma-thionin-like protein from roots of Norway spruce.";
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
putative plant defensin SPI1B.
putative plant defensin SPI1B.
pica abies (Norway spruce) (Picaa excelsa)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Picea abies (Norway spruce) (Picea excelsa)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea
                                                                                                                                                                        1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHK-CICYFPC 50
                                                                                                                                                                                                                               30 ELCKRESETWSGRCVNDYQCRDHCINNDRGNDGYCAGGYPWYRSCFCFFSC 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The purative gymnosperm plant defensin (SPII) accumulates agermination and a related SPIIB cDNA is found in needles."; Submitted (SEP-2002) to the EMBL/GenBank/DDBU databases.
                                                                                      20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X91487; CAA62761.1; -.
PIR; T14866; T14866.
HSSP; P41964; IMYN.
INCO. GO: 0003793; F: defense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
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83 AA; 8835 MW; B94207ADAB8FE4A5 CRC64;
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Last annotation update)
38.7%; Score 116.5; DB 1.
39.2%; Pred. No. 9.6e-08;
tive 10; Mismatches 20
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ProDom; PD002594; G_Purothionin; 1.
SMART; SM00505; Knotl; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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21; Conservative
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                    20; Conservative
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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"Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence features of the regions of 1,381,565 bp covered by twenty one physically assigned Pl and TAC clones.";
DNA Res. 5:131-145(1998).
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STRAIN=0V. Columbia;
MEDLINE=98344145; PubMed=9679202;
Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
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PubMed=11437247;
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P82789
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                                                                                                                                                                                                                                                                                                                                                                                                       Nicotiana tabacum (Common tobacco).
Bukaryota, Vitidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
Ismiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                       Gaps
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ezaki B., Yamamoto Y., Matsumoto H.; "Cloning and sequencing of the cDNAs induced by aluminium treatment and Pi starvation in cultured tobacco cells.";
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                                                                                                                                                                                      1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSC--NYVFPAHKCICYFPC
                                                                                                                        Score 115.5; DB 10; Length 83; Pred. No. 1.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101.5; DB 10; Length
Pred. No. 9.2e-06;
6; Mismatches 22; Indels
                                                                                                                                                       21; Indels
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GO, GO:003793; F:defense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                           SMART; SM00505; Knočl; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
SEQUENCE 83 AA; 8888 MW; E45BF9E61B9AA3D2 CRC64;
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64780A4984E371B0 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein LCR79 precursor.
                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                               83 AA
                                                                                                                      Query Match
38.4%; Score 115.5;
Best Local Similarity 42.0%; Pred. No. 1.3e
Matches 21; Conservative 7; Mismatches
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                                                                                                                                                                                                                                                                                                                               Created)
                           Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Physiol. Plantarum 93:11-18(1995).
WEBL; D29679; BAA06149.1; -. PIR; T03673; T03673.
HSSP; P30231; 1AYJ.
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ProDom; PD002594; G_Purothionin; 1.
InterPro; IPR008176; Gamma-thionin
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SEQUENCE 83 AA; 9700 MW; 6476
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                  IPR003614; Knot1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4097;
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Best Local S
                  nterPro;
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Matches
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Q40539
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P82788
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CV. Columbia;

MEDLINE=20083487; PubMed=10617197;

MEDLINE=20083487; PubMed=10617197;

MEDLINE=20083487; PubMed=10617197;

Buell C.Y., Kauls B., Roumsley S.D., Barnstead M.E., Feldblyum T.V.,

Buell C.Y., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Gronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vancosthuyse V., Miege C., Dumas C., Cock J.M.;

"Two large Arabidopsis thaliana gene familises are homologous to the Brassica gene superfamily that encodes poollen cast proteins and the male component of the self-incompatibility response.";

Plant Mol. Balol. 46.17-34(2001).

EMBL: ACO06223; -; NOT ANNOTATED CDS.

INTERPRO! FROOMST, ANNOTATED CDS.

INTERPRO! FROOMST, Gamma-thionin.

ProDom; PD002594; G Purcthionin; 1.

PROSTEE, PS00940; Gamma-thionin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 86.5; DB 10; Length 77; Pred. No. 0.0008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Indels
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
97194D61E5620DBE CRC64;
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein LCR80 precursor. LCR80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.7%;
38.0%;
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les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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72
69
89
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28
39
45
45
77 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum (Tomato).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamids, Solanales, Solanacees, Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Milligan S.B., Gasser C.S.;

Milligan S.B., Gasser 
Vanoosthuyse V., Miege C., Dumas C., Cock J.M.;
"Two large Arabidopsis thalliana gene families are homologous to the Brassica gene superfamily that encodes pollen coat proteins and that component of the self-incompatibility response.";
male component of the self-incompatibility response.";
plant Mol. Biol. 46:17-34[2001).
EMBL; ABOIL481; NOT_ANNOTATED_CDS.
GO; GO:0003793; Fiedefense/immunity protein activity; IEA.
Interpro; IPR003614; Knot1.
INTERPRO; SMOROS; Knot1.
Hypothetical protein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 KLCNGGLGNCGESC-NEQCCDRNCAQRYNGGHGYCNTLDDFSLCLCKYPC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KLCERSSGTWSGVCGNNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
27.7%; Score 83.5; DB 10; Length 108;
Best Local Similarity 32.0%; Pred. No. 0.0027;
Matches 16; Conservative 4; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q40128;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Flower-specific gamma-thionin-like protein/acidic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL 1 22 POTENTIAL.
CHAIN 23 108 HYPOTHETICAL PROTEIN LCR80.
SEQUENCE 108 AA; 11551 MW; 11E28E2CCE3578A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 26 POTENTIAL.
27 73 GAMMA-THIONIN-LIKE PROTEIN.
74 105 ACIDIC PROTEIN.
105 AA; 11914 MW; ADC9B7ECB620E814 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor
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SIGNAL
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C40128
AC C40128
DT C01-NO
DT 01-NO
DT 01-NO
DT 01-NO
DE FICWER
OC SEWRAT
OC LAMIN
RAN MILLI
RAN SAGNAR
R
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Search completed: May 11, 2004, 16:57:46 Job time : 41 secs

Title:

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33333
                                                                                                                                                                                                                        Score
                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                           May 13, 2004, 10:11:08 ; Search time 1734 Seconds (without alignments) 1249.799 Million cell updates/sec
                                                                                                                     301
1 KLCERSSGTWSGVCGNNNAC......QHGSCNYVFPAHKCICYFPC
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                          - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                        3470272 seqs, 21671516995 residues
                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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90-ba:*
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                                            OM protein
                                                                                                                                                                                                                        Searched:
                                                                                                                                   Seguence:
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                                                                 Run on:
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X97319 R.sativus m
AJ711046 Brassica
AF528180 Brassica
X97318 R.sativus m
AR014693 Sequence
AR432393 Sequence
                                                                                                                                                                                                                                                                              AR422382 Sequence
B34290 Phage and p
U18556 Raphanus sa
BD223233 Method of
BD240936 Polymucle
BD222337 Method of
BD222337 Method of
BD222337 Method of
BD14927 Disease t
AR014692 Sequence
AR43392 Sequence
AR43392 Raphanus sa
A26875 R.sativus A
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AB012871 Wasabia j
BV010712 MASC_STS1
BV010697 MASC_STS1
AC004747 Arabidops
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A63404 Sequence 19
AR050153 Sequence
AR130272 Sequence
E31545 Antibacteri
123728 Sequence 48
AR207337 Sequence
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BD174928 Disease t
AY060506 Arabidops
A68645 Sequence 13
X51916 A.thaliana
E31546 Antibacteri
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AR130280 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX412601 Sequence
                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                    Description
                                                                                                                                                                                                                                          A39553
                                                                                                                                           SUMMARIES
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AF528180
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AR130280
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AR050153
AR130272
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AX412601
AX651878
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AY060506
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AR432382
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AR432392
RSU18557
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I23728
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                                                                           em_htgo_hum:*
em_htgo_mus:*
em_htgo_other:*
                     htg_other:*
                              em_htg_mus:*
em_htg_pln:*
em_htg_rod:*
em_htg_mam:*
                                                     em_htg_we...
em_htg_vrt:*
       htg_hum:*
                htg_inv:*
                                                                                                                                                          Query
Match Length DB
em vi:*
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Sequence 58

Sequence 41

em_fun:
em_hum:
em_in:*
em_ou:*
em_or:*
em_ov:*

em_pat:* em_ph:* em_pl:* em_ro:*

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                                                                                                Brassica napus (rape)
Brassica napus
Brassica napus
Brassica napus
Brassica napus
Brassica napus
Spermatophyta; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 451)
Sohn,U., Lee,C.M., Lee,M.H. and Kim,J.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear PLN 31-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 AAGTIGTGCGAGAGGTCAAGTGGGACATGGTCAGGAGTCTTGGAAACAATAACGCCTGC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSEFP3
R. sativus mRNA for antifungal protein 3.
X97319.
X97319.1 GI:1655684
AFP; antifungal protein 3.
Raphanus sativus (radish)
Raphanus sativus (sadish)
Raphanus sativus
Raphanus Raphanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /noTe="transcript putatively induced by Screrotinia screrotium in infected Brassica napus"
                                                                                                                                                                                                                                           Unpublished 2 (bases 1 to 451)
Sohn, U., Lee, C.M., Lee, M.H. and Kim, J.H.
Direct Submission
Direct Submission
Sobmitted (29-MAY-1996) Department of Genetic Engineering,
Kyungpook National University, Puk-Ku, Sankyuk-Dong 1370,
                                                                                                                                                                                                                                                                                                                                                                  On Jul 1, 1996 this sequence version replaced gi:1293377, Location/Qualifiers
Brassica napus antifungal protein mRNA, complete cds.
U59459 H07366
U59459.1 GI:1399229
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50
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                   1. .451
/organism="Brassica napus"
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100.00%
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            LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.:
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Brassica oleracea def gene for defensin.
Brassica oleracea def gene for defensin.
AJ311046.
AJ311046.1 GI:13872713
def gene; defensin.
Brassica oleracea
Brassica oleracea
Brassica; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40
                                              Terras, F.R.G.
Direct Submission
Submitted (199-APR-11996) F.R.G. Terras, Institut fur
Pflanzenbiochemie, Stress- und Entwicklungsbiologie, Weinberg
Halle (Saale), D-06120, FRG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 AAGAATCAGTGCATTCGACTTGAAGGAGCACAACATGGATCTTGCAACTATGTGTTCCCT
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/dev_stage="adult plants infected with Alternaria brassicola"
Terras, F. R. G., Goderis, I. J., Penninckx, I. J., Osborn, R. W.
Broekaert, W. F.
Unpublished
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Conservative:
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/gene="AFP"
/product="antifungal protein 3"
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/gene="AFP"
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/gene="AFP"
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3NU59459

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2 (Park X.-S., Chung, S.-Y. and Cho, T.-J. Park X.-S., Chung, S.-Y. and Cho, T.-J. Direct Submission by Chung, S.-Y. and Cho, T.-J. Direct Submission of Life Sciences, Chungbuk Submitted (10-UUL-2002) Division of Life Sciences, Chungbuk National University, Gae-Shin-Dong San 48, Cheongju 360-763, Korea Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MAKFVSIITLFFAALVLFAAFEAPTMVKAOKLCERSSGTWSGVC"
                                                                    Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantaa, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
roside; eurosida II; Brassicales; Brassicaceae; Brassica.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Raphanus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 AAGAACCAGTGCATCAACCTTGAGGGAGCACGACATGGATCTTGCAACTATGTTTTCCCA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
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                                                                                                                                                                          Ryang,S.-H., Chung,S.-Y., Park,Y.-S. and Cho,T.-J.
Characterization of Chinese cabbage genes induced by Pseudomonas
syringae pv. tomato
Unpublished
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Broekaert,W.F.
Unpublished
     Brassica rapa subsp. pekinensis defensin mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                           organism="Brassica rapa subsp. pekinensis"
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Mismatches:
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AFP; antifingal protein 4.
Raphanus sativus (radish)
Raphanus sativus
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AF528180.1 GI:23321204
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Best Local Similarity:
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SONNACKNQCIRLBKARHGSCNYVFPAHKCICYFPC"
join 1366. 429,528. 5550)
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Submitted (24-APR-2001) Esnault R., Institut des Sciences
Vegetales, C.N.R.S., Avenue de la Terrasse, 91 198 Gif sur Yvette
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Mismatches:
Indels:
 Brassica oleracea def gene for defensin
Unpublished
2 (bases 1 to 933)
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1...829
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|gene="def"
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product="defensin"
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/gene="def"
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Unclassified.
1 (bases 1 to 285)
Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 05-DEC-1998
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                                                            'n
       Terwas, F.R.G.
Direct Submission
Submitted (09-APR-1996) F.R.G. Terras, Institut fur
Pflanzenbiochemie, Stress- und Entwicklungsbiologie, Weinberg :
Halle (Saale), D-06120, FRG
                                                                                                1. .499
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Matches:
Conservative:
Mismatches:
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Sequence 17 from patent US 5773696.
AR014693.1 GI:3972147
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Location/Qualifiers
1. 285
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44. .286
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/mol_type="unassigned DNA"

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Liang.J., Shah.D.M., Wu.Y.S. and Rosenberger,C.A.
Antifungal polypeptide AlyAFP from Alyssum and methods controlling plant pathogenic fungi
Patent: US 6653280-A 17 25-NOV-2003;
Location/Qualifiers
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Sequence 17 from patent US 6653280.
AR432393.1 GI:40194670
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Sequence 41 from Patent W09416076.
A39553
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                   unidentified
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Unbock, A.C., Powell, K.A. and Rees, S.B.
ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
Parent: WO 9416076-A 41 21-JUL-1994;
ZENECA LTD (GB)
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(Broekaert, W. F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 5824669-A 58 20-OCT-1998;
Location/Qualifiers
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                                                                                                                        Other publication AU 5820494 940815.
Location/Qualifiers
                                                                                                                                                               /organism="unidentified"
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Sequence 58 from patent US 5824869.
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/mol_type="unassigned DNA"
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A39553.1 GI:2295844
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                                                                   133 AAGTTGTGCCAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 192
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                                        21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyzValPhePro 40
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Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 553825-A 58 23-JUL-1996;
Location/Qualifiers
1. .288
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Brockaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: Use 6187904-A 58 13-FEB-2001;
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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Sequence 58 from patent US 5538525.
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E34290 bnA linear PAT 31-JAN-2002 Phage and plasmid constructed by ligating antibacterial protein gene DNA with vector DNA, transformant microorganism and transformant plant containing the same and antibacterial protein. E34290. I GI:18624295
DP 2000116379-A/1.
Unidentified unidentified unidentified unidentified unidentified unidentified. I (bases 1 to 449)
                                                                                                                                                                                                                                                                                                                                                                           159 AAGTIGTGCGAGAGTCCAAGTGGAACATGGTCAGGCGTGTGTGGGAAACAACAACGCTTGC 218
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Phage and plasmid constructed by ligating antibacterial protein gene DNA with vector DNA, transformant microorganism and transformant plant containing the same and antibacterial protein Patent: JP 2000116379-A 1 25-APR-2000;
TOYAWA PREF

SRaphanus sativus L.
PN JP 2000116379-A/1
PD 25-APR-2000
PP 09-OCT-1998 JP 1998288472
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C12N15/09,A01H5/00,A01N65/00,C07K14/415,C12N1/21,C12N5/10//
(C12N15/09,C12R1:91),(C12N1/21,C12R1:19),(C12N5/10,C12R1:91), F
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La (bases 1 to 308)

RS Liing, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.

Antifungal polypeptide AlvAPP from Alyssum and methods for controlling plant pathogenic fungi
NAL Patent: US 6653280-A 5 25-NOV-2003;
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Mol_type="genomic DNA"
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Unclassified.
1 (bases 1 to 308)
Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
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Patent: US 5773696-A 5 30-JUN-1998;
Location/Qualifiers
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Squence 5 from patent US 5773696.
AR014682. GI:3972136
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Sequence 5 from patent US 6653280.
AR432382. GI:40194659
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JOURNAL FEATURES

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us-10-006-252a-10.rge

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/mol type="mRNA"
/strain="ronde rode kleine witpunt"
/db_xref="taxon:3726"
/tisue_type="seed"
/tisue_type="seed"
/tisue_type="seed"
/gene="Rs-AFP2"
/gene="Rs-AFP2"
/gene="Rs-AFP2"
/gene="Rs-AFP2"
/gene="Rs-AFP2"
/gene="Rs-AFP2"
/gene="Rs-AFP2"
/gene="Rs-AFP2"
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/product="antifungal protein 2 preprotein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Rejection 457 bp mRNA linear PLN 07-JUL-1995
Rephanus sativus antifungal protein 2 preprotein (Rs-APP2) mRNA,
U18556.
U18556.1 GI:609319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, cosids, eurosids II, Brassicales, Brassicaceae, Raphanus.

1 (sites)

Terras, F.R.G., Eggermont, K., Kovaleva, V., Raikhel, N.V., Osborn, R.W., Kecter, A., Rees, S.B., Torrekens, S., Van Leuven, F., Vanderleyden, J., Cammue, B. P.A. and Broekaert, W.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission Submission Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory of Genetics, Applied Biological Sciences, W. De Croylaan 42, Heverlee, Belgium, B-3001 Location/Qualifiers
                                                                                                                                                                                            191 AAGAATCAGTGCATTCGACTTGAGAAAGCACGACATGGGTCTTGCAACTATGTCTTCCCA 250
                                                                                                                                                                                                                                                                             21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                           251 GCTCACAGTGTATCTGTTATTTCCCTTGT 280
                                                                                                                                                                                                                                                                                                                                                           41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                  Gaps:
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Plant Cell 7, 568-573 (1995)
2 (bases 1 to 457)
Terras,F.R.
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129. .281
/gene="Rs-AFP2"
                4.04e-27
                                 281.00
96.00%
92.00%
93.36%
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                                                    Percent Similarity:
Best Local Similarity:
Alignment Scores:
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                                                                                               Query Match:
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VERSION
KEYWORDS
SOURCE
ORGANISM
                Pred. No.:
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AUTHORS
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RSU18556
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/product="antifungal protein 2"
/function="antifungal, fungistatic"
/note="Evidence for antifungal activity: Analysis of two
novel classes of antifungal proteins from radish (Raphanus
sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
Chem. 267, 15301-15309"
                                                                                                                                                                                                                                                                                                                                         40
                                                                                                                                                                                                                                                                                                                                                                                     21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                          1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                              Gaps:
                                                                                                                   /evidence=experimental
                                                                                                                                                                                                                                                                                          US-10-006-252A-10 (1-50) x RSU18556 (1-457)
                                                                                                                                                                          4.12e-27
281.00
96.00%
92.00%
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Best Local Similarity:
Query Match:
DB:
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Search completed: May 13, 2004, 11:35:46 Job time: 1735 secs

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Brassica
Rs-AFP1 c
Antimicro
Raphanus
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Alyssum s
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Wasabia j
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A. thalia
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Amplified
                                                                                    Wasabia j
Brassica
                                                                                                             Wasabia j
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Cloned 3'
                                                                                                                                                                                                                                                                                                                                                                                                              Truncated
                                                                                                                                                             Arabidops
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                                 Aaq38650
Aaq70128
Aat72333
Aaz39123
AAc3123
AAC5123
AAG82691
                                                                                                                                                                                                                                                                                               Aaz99329
Aaz99333
Aaz99335
Aaz99338
Aaz99336
Aaz99336
Aaz99334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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AAQ38651
AAQ70129
AAZ99326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ38652 standard; DNA; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raphanus sativus.
RS-AFP2 CDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9305153-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1992;
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                                                                                                                                                                      AAQ38652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ38652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Command line parameters:
-MODEL=frame+ p2n, model -DEV=xlp
-MODEL=frame+ p2n, model -DEV=xlp
-MODEL=frame+ p2n, model -DEV=xlp
-Q=/Cgn2_1/USPTO spool p/US10006252/runat 11052004 141947 10940/app_query.fasta_1.199
-DB=N Geneseq_29\tilde{y}and4 -OPMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -STAFT=1 -END=-1 -MITRIX=bicsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRS=US1006522 @CGN 1 1 708 @runat 1105204 141947 10940 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMBOUT=120 -WARN TIMBOUT=30 -THRENDS=1 -XGAPPRT=0.5 -FGAPOP=6
-FGARFEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDEXT=7
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DNA encod
DNA encod
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DNA encod
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Aaq70130 Antimicro
Aat94577 Cloned 5'
                                                                               May 13, 2004, 09:41:12; Search time 349 Seconds (without alignments) 608.624 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                           1 KLCERSSGTWSGVCGNNNAC.....QHGSCNYVFPAHKCICYFPC 50
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Aat94577
Aaa53190 H
Aaz99324 I
Aaz51396 H
Aaz99327 I
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                             OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             3373863 segs, 2124099041 residues
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Listing first 45 summaries
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AAZ99327
AAZ99325
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AAA53190
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                                                                                                                                                                                             Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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genesequ2003as: *
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geneseqn2004s:*
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                     Run on:
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WO9416076-A1

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This cDNA represents the sequence of Rs-AFP2 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and digoxigenin-11-dUTP instead of further reamplified with the same primers and plaque hybridisation. Positive plaques were purified and subjected to two plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage R408.Inserts from 2 positive places were excised by Bcorl digstion and insert sizes of approx. 400bp the others between 250-300bp. The inserts of the 4 largest clones were then sequenced and found to differ only in the length of their S' and 3' UTR's. The longest sequence was identified as Rs-AFP1 so the Rs-AFP2 was seen to differ by only 2 amino acids from Rs-AFP1 so the Rs-AFP2 was seen to differ by only 2 amino acids incleotide sequence by PCR assisted site directed mutagenesis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                        Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial
                      Cammue BPA, Osborn RW, Rees SB, Terras FRG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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                                                                                                                                                                                                           Example 21; Fig 35; 110pp; English.
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                                                                                    WPI; 1993-100978/12.
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Best Local Similarity:
                      Broekaert WF, (
Vanderleyden J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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106 AAGTIGIGCCAAAGGCCAAGIGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; Rs-AFP2; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; PCR; polymerase chain reaction; mutagenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                 166 AAGAATCAGTGCATTAGACTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 225
                                                                                                                                                                                                                                                                                                                                                                      21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                              1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial Rs-AFP2.
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14-FEB-1995
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Raphanus sativus.

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Plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA sequence of PCR assisted site-directed mutagenesis of Rs-AFP2 is given in AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 AAGTIGIGCCAAAGCCCAAGIGGGACAIGGICAGGAGTCTGIGGAAACAAAAACGCAIGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LysleuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 LysAsnGlnCys1leArgleuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                          Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antifungal polypeptide, AlyAFP, inhibition, transgenic plants, phytopathogenic fungus, resistance, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 AlaHisLysCysIleCysTyrPheProCys 50
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                                                                                                                                                                                                                                                                                                        Disclosure; Page 33; 39pp; English.
                                                                                                                                                                 Dubock AC, Powell KA, Rees SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                 MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT94577 standard; DNA; 308 BP.
                                                                         94WO-GB000012.
                                                                                                       93GB-00000281
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                                                                                                                                                                                               WPI; 1994-249223/30.
                                                                                                                                     (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
                                                                                                                                                                                                               P-PSDB; AAR57327
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                                                                                                     08-JAN-1993;
                                                                       05-JAN-1994;
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                                           21-JUL-1994.
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Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
protein expression; plant defensin; RSAFP2; antifungal protein; AFP2; ss
                  Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance of rice paddy against pathogenic microbes.
                                                                                                          The present sequence encodes an antibacterial protein, designated radishin, isolated from Raphanus sativus (radish). A phage or plasmid comprising radishin can be used for increasing resistance of paddy and rice blast disease against pathogenic microbes
                                                                                                                                                                                                                                                                                                                                                                                     21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                    1 LysleuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAsnAlaCys
                                                                                                                                                                                   Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;
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448
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Matches:
Conservative:
Mismatches:
Indels:
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/*tag= a
/note= "encodes DmAMP1"
358. 510
/*tag= b
/note= "encodes RSAFP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                         US-10-006-252A-10 (1-50) x AAA53190 (1-449)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                  Claim 1; Page 4; 7pp; Japanese.
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                                                                                                                                                                                                                                     02e-26
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96.00%
92.00%
93.36%
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Best Local Similarity:
P-PSDB; AAY91117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dahlia merckii.
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04-DEC-1998;
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DB:
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ID AAZ
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                                                                                                                                                                                                                       This sequence is the product of the amplification of the 5' region of the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum, by a 5' RACE (Rapid Amplification of cDNA Ends) using primers AAF94575-T94576). The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCyaAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGTTGTGCGAGAGTCCAAGTGGAACATGGTCAGGCGTGTGTGGAAACAACAATGCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
pathogenic microbe; radish; rice blast disease; ds.
                                                                                                                                                 Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                G; 79 T; 0 U; 2 Other;
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344
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Matches:
Conservative:
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                                                                                         Rosenberger CA;
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                                96US-00627706
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281.00
94.00%
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                                                                                          Shah D, Wu
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                                                                                                                     WPI; 1997-503109/46.
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Best Local Similarity:
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                                                              (MONS ) MONSANTO
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                                                                                                                                                                                                                                                                                                                                                 Sequence 308
    27-MAR-1997;
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                                  29-MAR-1996;
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                                                                                          Liang J,
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Query Match:
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190 40

FILE MAY 14 09:4/:38 2004

99WO-GB002720

17-AUG-1999;

02-MAR-2000

Ray JA;

Evans 1J,

(ZENE) ZENECA LID. Evans IJ, Ray JA;

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The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMPP) I and the antifungal protein (AMPP). Inked by a linker propertied of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic and one basic residue as a cleavable linker sequence
                                                                                                                    Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
  De Bolle MFC,
                                                                                                                                                                                              Example 2; Fig 8; 151pp; English.
Broekaert WF, Francois IEJA,
                                           WPI; 2000-246564/21.
P-PSDB; AAY84057.
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Sequence 522 BP; 147 A; 119 C; 127 G; 129 T; 0 U; 0 Other;

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20
                                                                                                         1 LysieuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
            R 4 4 4 4 0 0 0
4 4
4 4
4 4
4
           Length:
Matches:
Conservative:
Mismatches:
Indels:
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           8.51e-26
281.00
96.00%
92.00%
                                Percent Similarity:
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Alignment Scores:
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RESULT 6

AAZ51396 standard; DNA; 534 BP 06-JUN-2000 AAZ51396;

(first entry)

Portion of pFAJ3106 encoding Dahlia merckii antimicrobial protein.

Antimicrobial protein; DmAMP; transgenic plant; microbial infection; bacteria; fungi; field crop; fruit; vegetable; canola; banana; sunflower; apple; plant transformation vector; ds.

Dahlia merckii. Synthetic.

Location/Qualifiers 76. .525 /*tag= a /product= "Antimicrobial protein"

WO200011196-A1

The present sequence corresponds to the region between XhoI and SacI sites of plant transformation vector pFAJ3106, which encompass the coding region for Dahlia merckii antimicrobial protein, Dm-AMPI. The vector is useful in the production of transgenic plants which show improved resistance to infections by microorganisms such as bacteria and fungi. Transgenic plants include e.g. field crops, fruits and vegetables, such as canola, sunflower, tomato, apple, banana, pear and mango ||||||||||:::||| 373 AAGTIGTGCCCAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 432 433 AAGAATCAGTGCATTAGACTTGAGAAAGCACGACATGGGATCTTGCAACTATGTCTTCCCA 492 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40 Antimicrobial protein; AMP1; transgenic plant; linker propeptide; protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss. Polynucleotide sequences and expression products useful for producing transgenic plants that are resistant to microbial infections. 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other; 534 22 00 00 DNA encoding a fusion protein of DmAMP1 and RSAFP2. Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: /*tag= a 162. .309 /*tag= b /note= "encodes DmAMP1" (1-534)Location/Qualifiers Example 3; Fig 7; 77pp; English. US-10-006-252A-10 (1-50) x AAZ51396 AAZ99327 standard; DNA; 534 BP 8.76e-26 281.00 96.00% 92.00% (first entry) WPI; 2000-237658/20. P-PSDB; AAY70323. Best Local Similarity: Synthetic. Dahlia merckii. Unidentified. Percent Similarity: Alignment Scores: misc_feature 03-JUL-2000 AAZ99327; Query Match: DB: ò à ò

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AAGAATCAGTGCATTAGACTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) and the antifungal protein 2 (APP2), linked by a linker propertied of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is posttranslationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
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Matches:
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372. .519
/*tag= c
/note= "encodes RSAFP2"
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                                                                                                                                                                                                                                                                                                                                                                                                   Francois IEJA,
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98GB-00026753
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Pred. No.:
     misc_feature
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04-DEC-1998;
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DB:
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The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein properties of the plant defensins, the Dahlia antimicrobial protein properties of the invention. The specification describes methods for the invention. The specification describes methods for expense of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is posttranslationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dispeptide; sequences consisting of either two addict, two basic or one
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protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 AAGTTGTGCCAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ray JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acidic and one basic residue as a cleavable linker sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evans IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                        /*tag= b
/note= "encodes DmAMP1"
370. .538
/*tag= c
/note= "encodes RsAFP2"
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                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 9; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Francois IEJA,
                                                                                                                                                                                                                                                                                                                                                                                        98GB-00018001.
98GB-00026753.
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96.00%
92.00%
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                                                                                                                                                                            .091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY84058
                                                           Synthetic.
Dahlia merckii.
Unidentified.
                                                                                                                                                                                                                                                                                          WO200011175-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Broekaert WF,
                                                                                                                                                                                                                                                                                                                                                           17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                          18-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-1998;
                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                            misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                           02-MAR-2000.
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Query Match:
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us-10-006-252a-10.rng

Conservative: Mismatches: Indels: Gaps: 96.00% 92.00% 93.36%

Percent Similarity: Best Local Similarity: Query Match: DB:

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(1-606)US-10-006-252A-10 (1-50) x AAZ99326

445 AAGTTGTGCCAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 504 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys ò

ઠે

41 AlaHisLysCyslleCysTyrPheProCys 50 원

RESULT 10 ABQ82690

ABQ82690 standard; cDNA; 243 BP.

ABQ82690;

(first entry) 02-JAN-2003 Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:1.

Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;

Eutrema wasabi

/product= "gamma-thionin" Location/Qualifiers 1. .243 /*tag= a

JP2002272292-A

24-SEP-2002

22-MAR-2001; 2001JP-00083526.

22-MAR-2001; 2001JP-00083526.

(IWAT-) IWATE KEN

WPI; 2002-718704/78. P-PSDB; ABP53725.

A disease-resistant plant in which wasabi gamma-thionin gene is introduced, creation of the disease-resistant plant,

Claim 3; Page 8; 11pp; Japanese.

The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence encodes a Eutrema wasabi (Wasabia japonica) gamma-thionin protein from the present invention

606 46

Length: Matches:

1.03e-25 281.00

Alignment Scores: Pred. No.: Score:

Sequence 243 BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 5.69e-26 279.00 96.00% 88.00% 92.69% Alignment Scores:

Percent Similarity:
Best Local Similarity:
Query Match:
DB:

0 4 4 4 0 0 0 4 4 6

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41 AlaHis 493 GCTCA 326 standa 326; L-2000 (f ncoding a icrobial r in expressetic. a merckii. ntified. ntified. 11175-Al. R-2000. G-1999; G-1999; C-1998;	(ZENE) ZENECA LTD. Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA; WPI; 2000-246564/21. P-PSDB; AAY84059.	Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit. Example 2, Fig 11; 151pp; English. The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) I and the antifungal protein 2 (AFP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region comprising a cleavage site, whereby the expressed polyprotein is post-translationally processed into the component protein molecules. The translationally processed into the component protein molecules. The propeptide sequences consisting of either two acidic, two basic or one acidic, and one basic residue as a cleavable linker sequence
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m 0 0

Mismatches: Indels:

92.00%

Gaps:

40

BP.

셤 ò QQ 8 q

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91 AAGTIGTGCGAGAGGCCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACAATAACGCATGC 150
                                                                                                                                                                                          1 LysleuCysCluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                    21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                                                                     211 GCTCACAAGTGTATTTGCTACTTCCCTTGT 240
                                                                                                                                                                                                                                               41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cammue BPA, Osborn RW,
                                                                 US-10-006-252A-10 (1-50) x ADC51221 (1-394)
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                                                                                                                                                                                                                                                                                                                                                         AAQ38650 standard; DNA; 414
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
 Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raphanus sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Broekaert WF, (
Vanderleyden J;
                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
07-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rs-AFP1 CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9305153-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-1992;
25-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                            AAQ38650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases.
              Query Match:
DB:
Local
                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                          AAQ38650
 Best
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                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                             40
                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
                                                                        91 AAGTTGTGCGAGAAAGTCAAGTGGGACATGGTCAGAGTCTGTGGAAACAACAATGCGTGC
                                                        LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                           21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Brassica oleracea defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                               antimicrobial protein; defensin; transgenic plant; composite disease resistance; pathogenic bacteria; rice white leaf blight, brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica oleracea defensin protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                                                                                                                                                                                      211 TATCACAGATGTATCTGTTACTTCCCATGT 240
                                                                                                                                                                                                41 AlaHisLysCysIleCysTyrPheProCys 50
                    US-10-006-252A-10 (1-50) x ABQ82690 (1-243)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 1; 34pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                          ADC51221 standard; DNA; 394 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-2001; 2001JP-00283117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-2001; 2001JP-00283117
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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P-PSDB; ADC51222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassica oleracea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP2003088379-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
                                                                                                                                                                                                                                                                                                                                              ADC51221;
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. .256 /*tag=

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This cDNA represents the sequence of Rs-AFPI from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for. screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFPI and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were exclsed in vivo into the pBluescript phagemid form with the aid of helper phage
                                                                                  of plants - e.g. brassica or resistance to fungal and bacterial
                                                                                       Biocidal proteins isolated from seeds dahlia, useful for increasing plants'
                                                                                                                                                                                                                                                                                                        Example 21; Fig 35; 110pp; English.
WPI; 1993-100978/12.
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394 46 1

Length: Matches: Conservative:

1.06e-25 279.00 94.00%

Percent Similarity:

Terras FRG;

Rees SB,

R408.Inserts from 22 positive clones were excised by EcoRI digestion and their size compared by agarose gel electrophoresis. Four clones had insert sizes of approx. 400bp the others between 250-300bp. The inserts of the 4 largest clones were then sequenced and found to differ only in the length of their 5' and 3' UTR's. The longest sequence is given here. (Updated on 25-MAR-2003 to correct PN field.) 8888888888

Other;

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0

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G; 132

80

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414 BP; 128 A; 74

correct PN field.)

Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

414 46 00 00 00 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.12e-25 279.00 94.00% 92.00% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB:

US-10-006-252A-10 (1-50) x AAQ38650 (1-414)

165 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 106 AAGTIGIGGGAAAGGCCAAGIGGGACAIGGICAGGAGICIGIGGAAACAAIAACGCAIGC Н ઠે g $\stackrel{>}{\circ}$

20 41 AlaHisLysCysIleCysTyrPheProCys

g ò 엄

GCTCACAAGTGTATCTGCTACTTTGT 255

RESULT 13

AAQ70128 standard; cDNA; 414 (revised)
(first entry) 25-MAR-2003 14-FFB-1995 AAQ70128;

Antimicrobial Rs-AFP1

Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.

Raphanus sativus.

WO9416076-A1

21-JUL-1994

94WO-GB000012. 05-JAN-1994;

93GB-00000281 08-JAN-1993;

(ZENE) ZENECA LTD

Powell KA, Dubock AC,

WPI; 1994-249223/30. P-PSDB; AAR57325 Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.

Disclosure; Page 31; 39pp; English

plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA sequence of Rs-AFP1 is given in AAQ70128. (Updated on 25-MAR-2003 to

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166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 225
                                                                                                                                40
                                                                                                                                                                                                                                                                                                           Antifungal protein; candida; fungal resistance; food additive; radish; crop protection; plant defensin; bacterial protection; preservative; ss.
                                                                                           LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                      106 AAGTIGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAAACAATAACGCATGC
                                                                                                                                21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                          /trag= a
/transl except= (pos:85. .87, aa:Glu)
16. .102
         414
46
1
3
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                                                                                                                                                                                                                                                                                           Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.
                          Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "antifungal_protein_1"
         Length:
Matches:
                                                                                                                                                                    50
                                                                                                                                                                                226 GCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                    41 AlaHisLysCysIleCysTyrPheProCys
                                                                        US-10-006-252A-10 (1-50) x AAQ70128 (1-414)
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                           AAT72333 standard; cDNA; 414
       1.12e-25
279.00
94.00$
92.00$
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/*tag= b
103. .255
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(first entry)
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                                     Similarity:
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                          Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9721815-A2
Alignment Scores
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19-JAN-1998
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                                             Query Match:
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(ZENE) ZENECA LTD.

95GB-00025455.

96WO-GB003068

12-DEC-1996; 13-DEC-1995; 28-MAR-1996; Meloen RH, Puijk WC, Schaaper WAM, Sijtsma L, Van Amerongen Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB; Van Gelder WMJ;

Ä,

WPI; 1997-332786/30. P-PSDB: AAW19280 Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.

```
This cDNA sequence encodes an Rhapanus sativus (radish) antifungal protein (Re-AFPI). Analogues of the homologous protein. Rs-AFPI) AAM19281, have also been produced (see AAM1928-92, AAM19294-98, AAM19301-04, AAM19330-34 and AAM31765-934). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease tolarance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct plied).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 AAGTIGIGGAAAGGCCAAGIGGGACAIGGICAGGAGICIGIGGAAACAAIAACGCAIGC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rs-AFP1; radish antifungal protein 1; fungicide; salt tolerance; preservative; transgenic plant; crop protection.
                                                                                                                                                                                                                                                                              Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
(trans1 except= (pos:85. .87, aa:Glu)
16. .102
                                                                                                                                                                                                                                                                                                                             414
944
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                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Radish antifungal protein 1 (Rs-AFF1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-006-252A-10 (1-50) x AAT72333 (1-414)
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              Claim 8; Fig 2; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-GB003065
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279.00
94.00%
92.00%
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103. .255
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
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                                                                                                                                                   New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                           Disclosure, Fig 2; 39pp; English
                                                      Broekaert WF, De Samblanx GW,
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279.00
94.00%
92.00%
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                                                                                           1997-332785/30.
                (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                P-PSDB; AAW19617
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods: IITLE OF INVENTION: Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
US-08-777-687-48

US-08-777-192-48

US-08-777-921-19

US-09-077-951-19

US-09-077-951-19

US-09-077-951-19

US-09-077-951-19

US-09-103-489-14

US-09-103-489-12

US-09-103-489-12

US-09-103-489-12

US-09-103-489-12

US-09-103-489-9

US-09-103-489-9

US-09-103-489-8

US-09-103-489-8

US-09-103-489-8

US-08-777-182-50

US-08-777-182-31

US-08-777-182-31

US-08-777-687-34

US-08-777-192-34

US-08-777-192-34
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ATTORNEY/AGENT INFORMATION:
NAME: CASTERATION CHARLES E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700) A
TELEPHONE: (314)537-6224
TELEPHONE: (314)537-6047
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/08627706
Patent No. 5773696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
 US-08-627-706-17
   RESULT 1
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-MODEL=frame+ p.D. model -DEV=xlp
-MODEL=frame+ p.D. model -DEV=xlp
-Q=/cgnz_1/USPTO_spool_p/US10006252/runat_11052004_141948_10973/app_query.fasta_1.199
-Q=/cgnz_1/USPTO_spool_p/US10006252/runat_11052004_141948_10973/app_query.fasta_1.199
-DB=1ssued_Patents NA -QFWT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEL-0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-MODE=LOCAL_GM=SOO -THR SCORE=pct -THR MINS_COO -ALIGN=15
-MODE=LOCAL -OUTFWT=pco -NORM=ext -HBAPSIZE=500 -MINLEN=0 -AAXLEN=200000000
-USRE=US10006252_GCGN 1 1 85 @runat 11052004 141948 10973 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THERAPSIZ=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPDP=6
-FGAPEXT=7 -YGAPDP=10 -YGAPEXT=0.5 -DELOPE=7
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17, Appl
58, Appl
58, Appl
58, Appl
55, Appli
5, Appli
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16, Appli
                                                                                                   May 13, 2004, 10:54:53; Search time 85 Seconds (without alignments) 326.442 Million cell updates/sec
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Sequence 2
Sequence 3
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Sequence 5
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Sequence 6
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1 KLCERSSGTWSGVCGNNNAC.....QHGSCNYVFPAHKCICYFPC
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11. /Ggn2_6/ptodact2/ina/5A_COMB.seq:*
12. /Ggn2_6/ptodact2/ina/5B_COMB.seq:*
31. /Ggn2_6/ptodact2/ina/6A_COMB.seq:*
41. /Ggn2_6/ptodact2/ina/6B_COMB.seq:*
42. /Ggn2_6/ptodact2/ina/PCTUS_COMB.seq:*
43. /Ggn2_6/ptodacta/2/ina/PCTUS_COMB.seq:*
44. /Ggn2_6/ptodacta/2/ina/PCTUS_COMB.seq:*
45. /Ggn2_6/ptodacta/2/ina/PcTUS_COMB.seq:*
46. /Ggn2_6/ptodacta/2/ina/Packfiles1.seq:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                      nucleic search, using frame_plus_p2n model
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US-09-103-489-17
US-09-2829-381D-17
US-08-377-687-58
US-08-777-192-58
US-08-777-192-58
US-08-627-706-5
US-09-103-489-5
US-09-829-381D-5
US-09-103-489-16
US-09-103-489-16
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                                                                                                                                                                                                                                                                                                                                                                                                                Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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length: 2000000000
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/desc = "synthetic DNA'

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; DESCRIPTION:
US-09-103-489-17
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APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: W. Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENIL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UN-1998
CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                     Gaps:
                     LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE: ocher nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
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TELEFAX: (314) 537-604
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
         SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
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Sequence 17, Application US/09829381D

Patent No. 6653280

GENERAL INFORMATION:
APPLICANT: Shah, Dilip M.
APPLICANT: Rescherger, Cindy A.
APPLICANT: Rescherger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: 18-201-04-09
CURRENT APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE PatentIn Version 3.1
                                                                                                                                                                                                                                                                            121 AAGTTGTGCCAAAGGCCATCAGGACTTGGTCAGGAGTCTGCGGAAACAACAACGGTGGC 180
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             Length:
Matches:
Conservative:
Mismatches:
Indels:
             Length:
Matches:
Conservative:
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Indels:
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                                                                                                                                            US-10-006-252A-10 (1-50) x US-09-103-489-17 (1-285)
                                                                                                                                                                                                                                                                                                                                                                  241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
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                                              Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-09-829-381D-17
Alignment Scores:
Pred. No.:
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Pred. No.:
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LENGTH: 285
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2444000
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REPRENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEBHONE: 202-861-300
TELEBHONE: 202-862-0944
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE GIRRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                   APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         SEE: CUSHMAN DARBY & CUSHMAN: 1100 NEW YORK AVENUE, N.W. WASHINGTON
                Sequence 58, Application US/08777192; Patent No. 5824869; GENERAL INFORMATION:
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281.00
96.00%
92.00%
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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Query Match:
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; LOCATION: 43.
US-08-777-192-58
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STATE: D.C.
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                         20005
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STREET: 11
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US-08-777-192-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 AAGTTGTGCCAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAAAAAAGCATGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LysasnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
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TLAINS CALLS

PRIOR APPLICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480

FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:
NAME: KOKULLS, PAUL N.

REGISTRATION NUMBER: 99042/SEE.36525/US/A

FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATICS:
LENGTH: 202-861-300

TELECOMMUNICATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                  ZUGNATION COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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         Sequence 58, Application US/08377687
Patent No. 5538525
GENERAL INFORMATION:
APPLICANT:
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBOXN, RUPERT W.
APPLICANT: OSBOXN, RUPERT W.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, TRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                       ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA
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281.00
96.00%
92.00%
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Query Match:
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LOCATION: 43.
US-08-377-687-58
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US-10-006-252A-10 (1-50) x US-08-627-706-5 (1-308)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO.: 5: SEQUENCE CHARACTERISTICS: LENGTH: 308 base pairs TYPE: mucleic acid STRANDEDNESS: single
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94.00%
92.00%
93.36%
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US-08-627-706-5
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971.982
FILING DATE: 17-NO. 6187904-1997
CLASSIFICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELERAK: 202-861-3000
TELERAK: 202-861-3000
TELERAK: 202-861-3000
TELERAK: 202-861-3000
TELERAK: 202-861-3000
TELENTH: 288 base pairs
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                   ADDRESSEE: CUSHWAN DARBY & CUSHWAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 GCTCACAAGTGTATCTGCTACTTTCCTTGT 282
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                                                                                                                                          REES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLEVENDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 43..282
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
                                 Sequence 58, Application US/08971982
Patent No. 6187904
GENERAL INFORMATION:
APPLICANT: BROEKABRT, WILLEM F.
CAMMUE, BRUNO P.A.
OSBORN, RUPERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.17e-28
281.00
96.00%
92.00%
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
RESULT 6
US-08-971-982-58
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21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
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US-08-627-706-5

JS-68-627-706-5

JS-68-627-706-5

JS-69-627-706-5

JS-69-627-706

JS-69-627-706

JS-69-627-706

JS-69-627-706

JS-69-627-706

JS-69-627-706

JS-69-627-706

JS-69-62-706

JS-69-62-70
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MEDIUM TYPE: Floppy disk
COMPUTER: TBW FC Compatible
COMPUTER: TBW FC COMPATIBLE
COMPUTER: TBW FC COMPATIBLE
COMPUTER: TBW FC COMPATIBLE
COMPARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILLING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: COhen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 34,565
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (314)537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-09-103-489-5
Sequence 5, Application US/09103489
Patent No. 6215048
Patent INFORMATION:
APPLICANT: Liang, Jihong
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159 AAGTIGIGGAGAGTCCAAGTGGAACATGGTCAGGCGTGTGTGGAAACAACAATGTTGC 218
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APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Why Younies
APPLICANT: Why Younies
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STRATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308
46
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic PCR reaction product FEATURE:
NAME/KEY: misc_feature
LOCATION: (22)..(248)
OTHER INFORMATION: N = any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-006-252A-10 (1-50) x US-09-829-381D-5 (1-308)
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Gaps:
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REFERENCE/DOCKET NUMBER: 38-21(10700)A
TELECOMMUNICATION:
TELEPHONE: (314)537-6224
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 5
LENGTH: 308
TUDEN TO 1
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Patent No. 5773696
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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281.00
94.00%
92.00%
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NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
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No.:
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Sequence 5, Application US/09829381D

Sequence 5, Application US/09829381D

Sequence 5, Application US/09829381D

Sequence 5, Applicant

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yonnie S.

APPLICANT: Wu, Yonnie S.

TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plante Pathogenic Fungi

FILE REFERENCE: 38-21 (10700) C

CURRENT APPLICATION NUMBER: US/09/829,381D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 AAGTIGIGCGAGAGTCCAAGTGGAACAIGGTCAGGCGIGIGGGAAACAACAAIGCTIGC
                       APPLICANT: Wu. Yonnie S.

PEPLICANT: Wu. Yonnie S.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F STERET: 700 Chesterfield Village Parkway No. 6215048th
                                                                                                                                                                                            ATTORNEY DATE OF COMPANY, BB4
STREET: 700 Chesterfield Village Parkway No. 62150
CITY: St. Louis
COUNTRY: USA
ZATE: Missouri
COUNTRY: USA
ZATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Flogby disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Flogby disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Flogby disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Plogby disk
COMPUTER: DATE OF MINION:
MAMB: COMBON CARTIES E.
REGISTRATION NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 38.21 (10700)A
TELEPONE: (314) 537-624
TELEPAN: (314) 537-637
TELEPAN: (314) 537-637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8044800
808
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 308 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281.00
94.00%
92.00%
93.36%
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US-09-103-489-5
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: W. Yonnie S.
APPLICANT: New Yonnie S.
APPLICANT: New Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Cohen, Monsanto Company, BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F STREET: 700 Chesterfield Village Parkway No. 6215048th CITY: St. Louis STATE: Missouri COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                    US-10-006-252A-10 (1-50) x US-08-627-706-16 (1-285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700) A.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6224

TELEPHONE: (314) 537-6224

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 285 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 AlaHisLySCySIleCySTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                      MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 16, Application US/09103489; Patent No. 6215048; GENERAL INFORMATION:
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 285 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                         5.69e-28
279.00
94.00%
92.00%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-09-103-489-16
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121 AAGTTGTGCGAGGGCCATCAGGGACTTGGTCAGGAGTCTGCGGAAACAACAACGATGC 180
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                                                                                                                                                                                 1 LysleuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                    285
1 1 6
0 0 0
                                                                      Length:
Matches:
Conservative:
Mismatches:
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                              241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
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                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: Synthetic US-09-829-381D-16
                                                                                 279.00
94.00%
92.00%
92.69%
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Best Local Similarity:
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Best Local Similarity:
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                                                            Alignment Scores:
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Pred. No.:
                                  US-09-103-489-16
                                                                                                                  Query Match:
DB:
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166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 225
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CLASSIFICATION:
PLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 199042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                         APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                 SSEE: CUSHMAN DARBY & CUSHMAN
1: 1100 NEW YORK AVENUE, N.W.
WASHINGTON
D.C.
IX: USA
                                                                                    Sequence 48, Application US/08777192
Patent No. 5824869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.24e-28
279.00
94.00%
92.00%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16..255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             20002
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-777-192-48
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CITY: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 AAGITGIGGGAAAGGCCAAGIGGGACAIGGICAGGAGICIGIGGAAACAAIAACGCAIGC 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/ABGIT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFRENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
TELECOMMUNICATION 1000
TELECOMMUNICATION 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
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                                                                         Sequence 48, Application US/08377687
Patent No. 5538525
GENERAL INFORMATION
APPLICANT BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: TERRAS, SARAH B.
APPLICANT: TERRAS, SARAH B.
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                          STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: 0.C. COUNTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.24e-28
279.00
94.00%
92.00%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
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Best Local Similarity:
Query Match:
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US-08-377-687-48
                                                           US-08-377-687-48
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Search completed: May 13, 2004, 12:19:39 Job time : 88 secs

RESULT 15

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15-56-571-900

15-56-571-900

US-10-006-252A-10 (1-50) x US-08-971-982-48 (1-414)

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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

9.24e-28 279.00 94.00\$ 92.00\$

Score: 2.
Percent Similarity: 9.
Best Local Similarity: 9.
Query Match: 3.

Alignment Scores: Pred. No.:

; NAME/KEY: CDS ; LOCATION: 16..255 ; SEQUENCE DESCRIPTION: SEQ ID NO: 48: US-08-971-982-48

TOPOLOGY: linear MOLECULE TYPE: cDNA FEATURE:

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both

41 AlaHisLysCysIleCysTyrPheProCys 50

BLOSUM62

Scoring table:

Perfect score:

Title:

Sequence:

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Run on:

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Total number

Searched:

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Sequence 13, Appl Sequence 2046, App Sequence 2046, App Sequence 15, Appl Sequence 21, Appl Sequence 14, Appl Sequence 12, Appl Sequence 9, Appl Sequence 9, Appl Sequence 8, Appl Sequence 8, Appl Sequence 283, Appl Sequence 283, Appl Sequence 34, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 15, Appl Sequence 11, Appl
Sequence 17, Appl
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Sequence 33, Appl
Sequence 6, Appli
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STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
                       13 US-10-681-972-17
9 US-09-759-584-58
9 US-09-829-381A-15
13 US-10-681-972-16
9 US-09-829-381A-16
13 US-10-681-972-16
9 US-09-928-847A-2046
14 US-10-10-527A-19
9 US-09-722-561-13
14 US-09-722-561-13
15 US-09-938-847A-2046
9 US-09-938-847A-2046
9 US-09-938-847A-2046
9 US-09-938-847A-2046
9 US-09-938-847A-2046
13 US-09-938-847A-2046
14 US-10-681-972-14
9 US-09-929-381A-12
13 US-10-681-972-12
9 US-09-829-381A-12
13 US-10-681-972-9
10 US-09-829-381A-8
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15 US-10-178-449A-48
15 US-10-178-449A-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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STATE: Missouri
COUNTRY: USA
ZIP: 63198
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          Command line parameters:
-MODEL=frame+-PD1.model -DEV=xlp
-MODEL=frame+-PD2.model -DEV=xlp
-MODEL=frame+-PD2.model -DEV=xlp
-DES-CGRL2 1/USPTO Spool p/US10006252/runat_11052004_141949_11000/app_query.fasta_1.199
-DES-PUBLIShed_App_lications_NA -QFNT=fastap_-SUFFIX=rnpb -MINMATCH=0.1
-LOOPELS -O. LOOPENXT=0 -UNITE=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_NIN=0 -ALIGN=15 -MODE=LOCAL -OUTFNT=PCO -THR_SCORE=pct -THR_MAX=100
-THR_NIN=0 -ALIGN=15 -MODE=LOCAL -OUTFNT=PCO -MOSN=ext -HEARSIZE=500 -MINLEN=0
-NGFUG= S. NO MMAR -LARGEQUERY N. NEG_SCORES=0 -WAIT -DSPBLOGX=100
-LONGLOG -DEV_TINEGUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOF=10 -XGAPOF=
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                                                                                                                                                                                                                            (without alignments)
68.324 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                           301
1 KLCERSSGTWSGVCGNNNAC.....QHGSCNYVFPAHKCICYFPC
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(GGNZ_6/ptodata1/pubpna/US07 PUBCOMB.seq:*

(GGNZ_6/ptodata1/pubpna/US06_PUBW_PUB.seq:*

(GGNZ_6/ptodata1/pubpna/US06_PUBCOMB.seq:*

(GGNZ_6/ptodata1/pubpna/US07_NEW_PUB.seq:*

(GGNZ_6/ptodata1/pubpna/US07_NEW_PUB.seq:*

(GGNZ_6/ptodata1/pubpna/US08_PUBCOMB.seq:*

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                                                                                                                                                                                              ; Search time 3321 Seconds
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                     nucleic search, using frame plus p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                           May 13, 2004, 11:00:48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seg length: 0
Maximum DB seg length: 200000000
                                                                                                                                                                                                                                                                                                                             US-10-006-252A-10
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MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

SUMMARIES

Database

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DB

Query Match Length

Score

Result No.

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121 AAGTIGIGECAAAGGCCATCAGGGACTIGGTCAGGAGTCTGCGGGAAACAACAACAAGGCATGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM CM COMPUTER: US/09/759,584

FILING DATE:

APPLICATION NUMBER: US/09/759,584

FILING DATE:

APPLICATION NUMBER: 08/377,687

FILING DATE:

APPLICATION NUMBER: 16,773

REGISTRATION NUMBER: 16,773

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 16,773
                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                    US-10-006-252A-10 (1-50) x US-10-681-972-17 (1-285)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 58, Application US/09759584
; Sequence 58, Application US/09759584
; Patent No. US2001014732A1
; APPLICANT: BROEKARRT, WILLEM F., APPLICANT: CAMMUB, BRUNG P.A., APPLICANT: CAMMUB, RUEBER W., APPLICANT: REES, SARAH B., APPLICANT: TERRAS, FRANKY R.G., APPLICANT: TERRAS, FRANKY R.G., APPLICANT: TERRAS, FRANKY R.G., APPLICANT: VANDERLEYDEN, JOZEF TITLE OF INVENTION: BIOCIDAL PROTEINS NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN NATHER.
                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
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TELEPHONE: 202-861-3000
            , OTHER INFORMATION: Synthetic US-10-681-972-17
                                                                                                                                                     281.00
96.00%
92.00%
93.36%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity:
                                                                                                Alignment Scores:
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JOSEURON 10. US20040064850A1

GENERAL INFORMATION:

GENERAL INFORMATION:

JAPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yonnie S.

JILLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi

FILE REFERENCE: 38-21 (10700) C.

CURRENT APPLICATION NUMBER: US/09/829,381D

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Plant OF DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Petentin Version 3.1

LENGTH: 285

TEMPER: DAA

CREATURE:

CREATUR
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121 AAGTTGTGCCAAAGGCCATCAGGACTTGGTCAGGAGTCTGCGGAAACAACAACGATGC 180
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-829-381A-17
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
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96.00%
92.00%
93.36%
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Percent Similarity:
Best Local Similarity:
Query Match:
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Query Match:
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                                                                                                                                                                                                                                                                                                                             21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
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CORRESPONDENCE ADDRESSE:
Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                  1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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APPLICATION NUMBER: US/09/829,381A

FILING DATE: 09-Apr-2001

CLASSIFICATION NUMBER: US/09/829,381A

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNEY/AGENT INFORMATION:

NAME: COHO: Charles E.

REGISTRATION NUMBER: 34.565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A

TELECHONE: (314) 537-6047
                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                            US-10-006-252A-10 (1-50) x US-09-759-584-58 (1-288)
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LENGTH: 308 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: LINEAR

MOLECTLE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-829-381A-5
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Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS
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                                                                                           281.00
96.00%
92.00%
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  43..282
                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                        Alignment Scores:
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US-09-829-381A-5
LOCATION:
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US-09-759-584-58
                                                                            Pred. No.:
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VG-10-68-972-5

VG-10-68-972-7

VG-10-68-7

VG-10-
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                                                                                                                                                                                                                                                                                                                                           1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
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Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                      US-10-006-252A-10 (1-50) x US-09-829-381A-5 (1-308)
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ORGANISM: Artificial Sequence
                         7.7e-31
281.00
94.00%
92.00%
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281.00
94.00$
92.00$
                                                                           Percent Similarity:
Best Local Similarity: 5
Query Match:
DB:
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US-10-681-972-5
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Best Local Similarity:
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Pred. No.:
Alignment Scores:
Pred. No.:
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ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: D.C.
COUNTRY: USA
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                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: Charles B. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yomie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285
46
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APPLICATION NAMER: 09/103,489

ALING DATE: 1998-06-24

ATTORNEY/AGENT INFORMATION:
NAME: COREN, Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: (desc = "synthetic DNA" SEQUENCE DESCRIPTION: SEQ ID NO: 16:
241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (114) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                              Sequence 16, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.346-30
279.00
94.00%
92.00%
                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                    US-09-829-381A-16
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                 279
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DB:
                                                  RESULT 6
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Sequence 16. Application US/10681972

| Sequence 16. Application US/10681972
| Publication No. US20040064850A1
| GENERAL INFORMATION:
| APPLICANT: Liang, Jihong
| APPLICANT: Shah, Dilip M.
| APPLICANT: Shah, Dilip M.
| APPLICANT: Rosenberger, Cindy A.
| TITLE OF INVENITON: Plant Pathogenic Fungi
| TITLE OF INVENITON: NUMBER: US/10/681,972
| CURRENT APPLICATION NUMBER: US/09/829,381D
| PRIOR APPLICATION NUMBER: US/09/829,381D
| PRIOR PILING DATE: 1998-06-24
| WINGER OF SEQ ID NOS: 20
| NUMBER OF SEQ ID NOS: 20
| OFFICE OFFIC
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: SECURRAS, STANKY R.G.
ANDERS OF SECURACES: 59
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: CUSHWAN DARBY & CUSHWAN STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/09759584 Patent No. US20010014732A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.34e-30
279.00
94.00$
92.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Synthetic US-10-681-972-16
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Percent Similarity:
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US-10-006-252A-19
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Pred. No.:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAhaCys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 LysAsnGlnCysileArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4146
1200
4146
000
                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REPERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPHONE: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION:
APPLICATION:
APPLICATION:
APPLICATION NUMBER: 08/377,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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Publication No. US20030226169A1
GRNERAL INFORMATION:
APPLICANT: Van Amerongen, Aart
APPLICANT: Fant, Franky
APPLICANT: Borremans, Frans
APPLICANT: Borremans, Frans
APPLICANT: Sijisma, Lolke
APPLICANT: Sijisma, Lolke
APPLICANT: Sijisma, Lolke
APPLICANT: Broekert, Wilhelmus
APPLICANT: Broekert, Wilhelmus
APPLICANT: Broekert, Wilhelmus
APPLICANT: Broekert, Wilhelmus
APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Rees, Sarah
ITILE OF INVENTION: Attifungal Proteins
ITILE OF INVENTION ATTICATION NUMBER: US/10/388,361A
CURRENT FILING DATE: 2003-03-13
CURRENT FILING DATE: 2003-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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PRIOR FILING DATE: 1998-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.19e-30
279.00
94.00$
92.00$
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ), NAME/KEY: CDS
; LOCATION: 16..255
US-09-759-584-48
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Best Local Similarity: 9
Query Match:
DB:
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1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-006-252A-10 (1-50) x US-10-388-361A-45 (1-414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/10006252A

Sublication No. US20020152498A1

GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Rees, Sarah
ITILE OF INVENTION: Antifungal Proteins
ITILE REFERENCE: STN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US/077,951
PRIOR FILING DATE: 1996-06-10
PRIOR FILING DATE: 1996-12-13
SEIGN FILING DATE: 1996-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
PRIOR APPLICATION NUMBER: PCT/GB96/03068
PRIOR FILING DATE: 1996-12-12
PRIOR APPLICATION NUMBER: GB 9606552.9
PRIOR PILING DATE: 1996-03-28
PRIOR PILING DATE: 1996-03-28
PRIOR PILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 45
LENGTH: 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AlaHisLysCysIleCysTyrPheProCys 50
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Gaps:
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279.00
94.00%
92.00%
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                                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Raphanus sativus
US-10-388-361A-45
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Best Local Similarity:
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165

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US-U9-938-844A-2046
) Sequence 2046, Application US/09938842A
) Sequence 2046, Application US/09938842A
) Patent No. US202020160378A1
) GENERAL INPORMATION:
APPLICANT: Harper, Joef
APPLICANT: Mang, Xun
APPLICANT: Wang, Xun
APPLICANT: SCRIP1300-3
CURRENT TILING DATE: 2001-06-24
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR PILING DATE: 2001-06-24
PRIOR PILING DATE: 2001-06-24
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2046

LENGTH: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2046, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                      116 AAGTTGTGCGAGGGCCAAGTGGGACATGGTCCGGAGTTTGCGGAAACAGTAACGCGTGC 175
                                                                                           21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys 20
                                                                        21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                              236 GCTCACAATGTATCTGCTACTTCCCATGT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 GCACACAAGIGIAICIGITACGICCCAIGI 240
                                                                                                                                               41 AlaHisLysCysIleCysTyrPheProCys 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272.00
94.00%
88.00%
90.37%
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US-09-938-842A-2046
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166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGGATCTTGCAACTATGTCTTCCCA 225
                                                       40
                                                       LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
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O N
W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
PRIOR APPLICATION NUMBER: 00/10672
FILING DATE: 20-JUN-1997
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
RESTSTRANGY/DOCKET NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                     226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                            41 AlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSER: ZENECA AG Products
STREET: 1800 Concord Pike
CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 403 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274.00
94.00%
90.00%
91.03%
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE
USA
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Pred. No.:
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us-09-732-561-15
; Sequence 15, Application US/09732561
; Patent No. US2002035738A1
; GENERAL INFORMATION:
APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
APPLICANT: Penninckx, Iris
APPLICANT: Razan, Kemal
; APPLICANT: Razan, Kemal
; APPLICANT: Brockart, Willem
ITTLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADBESSEE: ZENECA AG Products
STREET: 1800 Concord Pike
CITY: Wilmington
STREET: DE
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-006-252A-10 (1-50) x US-09-938-842A-2046 (1-243)
                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: S379
LENGTH: 243
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/202,638
APPLICATION NUMBER: 05/202,638
APPLICATION NUMBER: 20-2031/01672
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                      1.08e-29
272.00
94.00%
88.00%
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Best Local Similarity:
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US-09-732-561-15
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182 AAGAATCAGTGCATTAACCTTGAAGGAGCCAAAACATGGATCATGCAACTATGTCTTCCCA 241
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                                                                                                                                                                                                                                                                                                                                   1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
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                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                          US-10-006-252A-10 (1-50) x US-09-732-561-15 (1-400)
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 GCACACAAGIGIAICIGIIACGICCCAIGI 271
                                                                                                                                                                                                                                                                                                                                                                                                                                       41 AlaHisLysCysIleCysTyrPheProCys 50
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ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(400)
OTHER INFORMATION: n = A,T,C or
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US-09-887-576-607
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Score: 272.00
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Best Local Similarity: 88.00%
Query Match: 90.37%
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US-10-006-252A-10 (1-50) x US-09-887-576-607 (1-400)

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Search completed: May 13, 2004, 13:15:13 Job time : 3323 secs g

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29: gb_gss2:*
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1 KLCERSSGTWSGVCGNNNAC.....QHGSCNYVFPAHKCICYFPC 50
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                 OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygappp 10.0, Ygapext
Fgappp 6.0, Fgapext
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Database :

CA992140 HC0577 GIECOBRL CAT. NO. 19643-014 Brassica rapa subsp. rekinensis			kinensis	kinensis	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	assicales; Brassicaceae; Brassica.
	cDNA, mRNA sequence.	CA992140.1 GI:37621435	EST. Brassica rapa subsp. pekinensis	Brassica rapa subsp. pekinensis	Eukaryota, Viridiplanta	Spermatophyta; Magnolic	rosids; eurosids II; Br
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E 1 (bases 1 to 346)
S Gao.R.J., Dai, D.P. and Ma.R.C.
Expressed sequence tags of heading leaf during the heading process of Chinese cabbage
Of Chinese cabbage
Unpublished (2003)
Contact: Rongaci, Ma
Plant Functional Genomics
Beijing AgroBiotechnology Research Center
Haidian District, Ban-Jing Rd., Beijing 100089, China
Tel: 86 10 5150 3831
Fax: 86 10 5150 3831
Fax: 86 10 5150 3800
Email: romal@yahoo.com
Seq primer: T7
High quality sequence stop: 346
POLXA=No.
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BN40.062L22F011227 BN40 Brassica napus cDNA clone BN40062L22, mRNA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
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BN45.043G08F011229 BN45 Brassica napus CDNA clone BN45043G08, mKNA
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Brassica napus
Brassica napus
Brassica napus
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).
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John Transplante Rochefort 91025 EVRY CEDEX France 93, rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00

Rax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).

Location/Qualifiers

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/clone="BN40065MOS"
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     201 AAGAATCAGTGCATTCGACTAGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 260
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Contact: Genoplante
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CD833047.1 GI:32514987
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Brassica napus (rape)
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CD831226
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                                                                                                                                                                                                                                                                                                                                                                                               CD833613 427 bp mRNA linear EST 10-JUL-2003 BN40.067P16F011228 BN40 Brassica napus CDNA clone BN40067P16, mRNA
                                                                                                                                                             Brassica napus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
1 (bases 1 to 427)
Genoplante.
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751: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Contact: Genoplante
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/organism="Brassica napus"
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/db xref="taxon:3708"

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/t.ssue type="seed"

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CD833613
CD833613.1 GI:32515553
               8.18e-23
284.00
96.00%
94.00%
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Best Local Similarity:
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SOURCE

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CD833784 476 bp mRNA linear EST 10-JUL-2003 BN45.001122F010914 BN45 Brassica napus cDNA clone BN45011122, mRNA
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 plant genomics programme 'Genoplante' (http://www.genoplante.com
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Contact: Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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             and http://genoplante-info.infoblogen.fr/
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Mismatches:
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Matches:
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                                                                         organism="Brassica napus"
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                                 Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta,
Papermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
(bases 1 to 457)
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                                                                                                                                                                                              93, rue mari Rochefort 91025 EVRY CEDEX France
721: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Brassica napus (rape)
Brassica napus
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Brassica napus
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
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Tel: 33 1 69 47 54 00
Fax: 31 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                  1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                         160 AAGTIGIGGGGGCCAAGTGGGACATGGTCAGGAGTTTGTGGAAACAATAATGCGTGT
                                                                                                                                                                          21 LysAsnGlnCys1leArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                             220 AAGAATCAGTGCATTCGACTTGGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA
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                                                                                                                                                                                                                                                        280 GCTCACAAGTGTATCTGCTATTTCCCTTGT 309
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EST.
Brassica napus (rape)
Brassica napus
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CD834092
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CD433924 481 bp mRNA linear EST 10-JUL-2003
BN45.040A03F011018 BN45 Brassica napus cDNA clone BN45040A03, mRNA
sequence.
                                                                                                                                                                                       Brassica napus (rape)
Brassica napus
Brassica napus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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482 bp mRNA linear EST 10-JUL-2003 BN45.001A11F010914 BN45 Brassica napus cDNA clone BN45001A11, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                 93. The Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                                                                    Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="Rn4504030"
/tissue_type="seed"
/clone_lib="BN45"
41 AlahisLysCysIleCysTyrPheProCys 50
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                                                                                                                                     CD833924.1 GI:32515864
EST.
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CD833627.1 GI:32515567
EST.
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284.00
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94.00%
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Brassica napus
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Genoplante.
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Best Local Similarity:
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Pred. No.:
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CD833924
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CD833627
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CD628840
BN40.040A23F011019 BN40 Brassica napus CDNA clone BN40040A23, mRNA sequence.
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1 (bases 1 to 543)
Genoplante.
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                                                                                                                                                                                                                                                                                                                                                                                                                                21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93, run Hornes Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
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Conservative:
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Matches:
Conservative:
Mismatches:
                                    /organism="Brassica napus"
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/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="RNA5001C04"
/tissue_type="seed"
/clone_lib="BN45"
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/mol_type="mRNA"
/cultivar="Jet neuf"
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/clone="BN40040A23"
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/clone_lib="BN40"
       Location/Qualifiers
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Brassica napus
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BN45.001C04F010914 BN45 Brassica napus cDNA clone BN45001C04, mRNA
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1 (bases 1 to 523)
Genoplante
Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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Fax: 33 1 69 47 54 10

Fax: 33 1 69 47 54 10

Fits sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                              73. The Henri Rochefort 91025 EVRY CEDEX France
1781: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
                                                                               Genoplante.

Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
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Conservative:
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Indels:
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/cultivar="Jet neuf"
/db xref="taxon:3708"
/clone="RN45001All"
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/clone_lib="BN45"
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96.00$
94.00$
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Brassica napus
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Genoplante
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Best Local Similarity:
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BN40.046D16F011221 BN40 Brassica napus CDNA clone BN40046D16, mRNA
                                                                                                   201 AAGAATCAGTGCATTCGACTAGAGAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 260
                                                                                                                                                                                                                                                                                                                                                                                                     Eukarrocta "Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; cosids; eurosids II; Brassicales; Brassicaceae; Brassica. [Genoplante.]
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Contact: Genoplante
                                                                                  LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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/organism="Brassica napus"
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/clone_lib="BN40"
                                                                                                                                                                                                                         GCTCACAGAGTGCATCTGCTACTTCCCTTGT 290
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                Indels:
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CD830628.1 GI:32512568
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Brassica napus
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284.00
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Best Local Similarity:
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CD829429

BN40.042B06F011226 BN40 Brassica napus CDNA clone BN40042B06, mRNA sequence.
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,

rosids, eurosids II; Brassicales; Brassicaceae, Brassica.

1 (Sases I to 646)

Genoplante.
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Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                         93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Brassica napus"
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255 GCTCACAGTGCATCTGCTACTTCCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol type="mRNA"

/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40042B06"
/tissue_type="seed"
/clone=lib="BN40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-006-252A-10 (1-50) x CD829429 (1-646)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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EST.
Brassica napus (rape)
Brassica napus
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Pred. No.:
                    261
                                                                                              DEFINITION
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AUTHORS
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COMMENT
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CD829429
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KEYWORDS
SOURCE
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- protein search, using frame_plus_n2p model

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Run

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1586107 seqs, 282547505 residues

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BLOSUM62 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

US-10-006-252A-19 752

Perfect score:

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                                          Aaw40351 Aaw40351 Aaw40351 Aaw40346 Aaw40346 Aay57565 Aaw40345 Aaw40345 Aaw40349 Aaw403349 Aaw603349 Aab607317 Aab60730 Aab607030 Aab607
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Aae10625
Aaw40347
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AAW40349
AAY00738
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AAW40347
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ABP81292
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(first entry)
Broekaert WF, Cammue
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07-JUL-1993
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AAR33706;
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Aar33706 Antifunga
Aaw57325 Antimicro
Aaw19280 Raphanus
Aaw19617 Radish an
Aar33708 Antifunga
Aar57327 Antimicro
Adc51222 Brassica
Aay91117 Raphanus
Aay91117 Raphanus
                                                                                             May 11, 2004, 16:57:25 ; Search time 59.5 Seconds (without alignments) 3931.922 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES

DB

Length

Query Match

Result Š.

A Geneseq 29Jan04:*
2: geneseqp1980s:*
2: geneseqp2000s:*
3: geneseqp2001s:*
5: geneseqp2001s:*
5: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*

AAR33706 AAR57325 AAW19617 AAW33708 AAR57327 ADC51222 ADC51222 AAY91117 AAY84072

880 880 880 880 880

2 6 4 5 9 7 8 6 0 1

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136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
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                                                                       This sequence is antifungal protein Rs-AFP1 from Raphanus sativus. The exact source and isolation of the encoding DNA sequence is unclear from the specification. The protein is useful for combating fungi or bacteria eg gram positive bacteria and plant pathogenic fungii. It has moderate sensitivity to ions and an apparent low toxicity for cultured human cells. Plants transformed with the encoding DNA show increased disease resistance. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                   21 PheGlualaproThrMetValGlualaGlnLysLeuCysGluArgProSerGlyThrTrp 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG
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Matches:
Conservative:
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Indels:
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                                                  Disclosure; Fig 35; 110pp; English
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N-PSDB; AAQ70128.
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Query Match:
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                                                                          plant-derived antimicrobial proteins are expressed in endosymbiotic clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFPI from R. sativus. The full-length cDNA sequence of Rs-AFPI is given in AAQ70128, and the amino acid sequence predicted from this sequence in AAR57325. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antifungal protein; candida; fungal resistance; food additive; radish; crop protection; plant defensin; bacterial protection; preservative.
                                                                                                                                                                                                                                                                                                                                                                     76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
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Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
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13. .80
/label= antifungal_protein_1
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                                                      Disclosure; Page 32; 39pp; English
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96GB-00006552.
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28-MAR-1996;
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19-JAN-1998
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Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 PheGludladaGluThrMetValGludAlaGlnLysLeuCysGludrgProSerGlyThrTrp 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sijtsma L, Van Amerongen A;
Borremans FAM, Rees SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             salt tolerance;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
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                                             Puijk WC, Schaaper WMM,
, Samblanx GW, Fant F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Radish antifungal protein 1 (Rs-AFP1).
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                                                                                                                                                                                                                         Claim 1; Fig 2; 65pp; English.
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434.00
98.75%
98.75%
57.71%
                                                                                                            1997-332786/30.
             (ZENE ) ZENECA LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
Query Match:
                                                                                                                            N-PSDB; AAT72333
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                                                                              Van Gelder WMJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 AA;
                                Meloen RH, Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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This polypeptide comrpsies the preprotein for radish antifungal protein I (RS-AFP1). Novel antifungal proteins are based on Rs-AFP1, Rs-AFP2 (see AAW1916). NS-AFP3 and Rs-AFP4, especially those in which Gly9 is repaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met. Mutants (see AAW26371-90) of Rs- AFP2 are specifically claimed. The mutants show improved salt tolerant antifungal activity, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135
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                                                                                                                                                                                                                                                                                                 New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                         30. .80
/label= Mat_protein
/note= "RSAFP1"
Location/Qualifiers
1. .29
                       /label= Pro-peptide
                                               'note= "encoded by
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                                                                                                                                                               96WO-GB003065.
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434.00
98.75%
98.75%
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(first entry)
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                                                                                                                                                                                                                                                               WPI; 1997-332785/30.
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Best Local Similarity:
Query Match:
DB:
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                                   Misc-difference
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                                                                                                                                                                                                           (ZENE ) ZENECA
                                                                                                                                                                                                                                       Broekaert WF,
                                                                                                                                                                                     13-DEC-1995;
                                                                                                                                                             12-DEC-1996;
                                                                                                             WO9721814-A1
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                                                                                                                                    19-JUN-1997
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07-JUL-1993
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Key
Peptide
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AAR33708
ID AAR3
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AC AAR3
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DT 25-M
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Antimicrobial, Rs-AFP2; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; PCR; polymerase chain reaction; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant-derived antimicrobial proteins are expressed in endosymbiotic clavibacter xyli subsp. cynodomis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA sequence of PCM assisted atte-directed mutagenesis of Rs-AFP2 is given in AAAC70130 and the deduced amino acid sequence in AAR57127. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial protein producing endo-symbiotic microorganisms - is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 33-34; 39pp; English.
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                                                                                                                                                                                                                                                                                                                                    94WO-GB000012.
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433.00
98.75%
97.50%
                                        (first entry)
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                    (revised)
                                                                                 Antimicrobial Rs-AFP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-249223/30.
                                                                                                                                                                                                                                                                                                                                                                                                                      (ZENE ) ZENECA LTD.
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                                                                                                                                                                                                             Raphanus sativus.
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                                                                                                                                                                                                                                                                                                                                    05-JAN-1994;
                    25-MAR-2003
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                                        14~FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is part of antifungal protein Rs-AFP2, decoded from a mutaganised RsAFP1 clone derived from Raphanus sativus. The protein is useful for combating fungi or bacteria eg gram positive bacteria and plant pathogenic fungii. It has moderate sensitivity to ions and an apparent low toxicity for cultured human cells. Plants transformed with the encoding DNA show increased disease resistance. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
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                                                      Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cammue BPA, Osborn RW, Rees SB,
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                    92GB-00003038.
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                  Antifungal protein Rs-AFP2.
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98.75%
97.50%
57.58%
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                                                                                                                                              Raphanus sativus.
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                                                                                                                                                                                    WO9305153-A1
                                                                                                                                                                                                                                                                     27-AUG-1992;
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Query Match: DB: Best Local

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TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                                                                                                                                   16 ATGCCTAAGTTTGCGTCCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTGCTGCT
                                                            Conservative:
Mismatches:
Indels:
Length:
Matches:
                                                                                                                                                                   Gaps:
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AAR57327;

AARS7327 ID AARS XX AC AARS RESULT 6

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ADC51224 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAGGAGICTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGACATGGATCTTGCAACTATGTCTTCCCAGCTCAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present amino acid sequence represents a Brassica defensin protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp
                                                                                  antimicrobial protein; defensin; transgenic plant; composite disease resistance; pathogenic bacteria; rice white leaf blight; brown stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          002028
                                                                                                                                                                                                                                                                                                                                   (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
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Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1-80)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 2; 34pp; Japanese.
                                                          Brassica oleracea defensin protein.
                                                                                                                                    seedling damping-off disease; filam
sheath blight disease; leaf blight.
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                                                                                                                                                                                                                                                                        18-SEP-2001; 2001JP-00283117.
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432.00
97.50%
97.50%
                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                 2003-621123/59
                                                                                                                                                                                Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-621123/
N-PSDB; ADC51221.
                                                                                                                                                                                                             JP2003088379-A.
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                              18-DEC-2003
                                                                                                                                                                                                                                             25-MAR-2003.
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ADC51222;
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ADC51224
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Score:

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Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases stripe disease, backen bight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present amino acid sequence represents a Brassica defensin protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGGAGICTGIGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
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                                                                                                                                                                                                                            composite disease resistance; pathogenic bacteria; rice white leaf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight
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                                                                                                                                                                                                 antimicrobial protein; defensin; transgenic plant;
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
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425.00
96.25%
96.25%
56.52%
                                                                                               (first entry)
                                                                                                                                                Brassica defensin protein.
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N-PSDB; ADC51223.
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                                                                                               18-DEC-2003
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                                           ADC51224;
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135

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75 20 195

255

80

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Antimicrobial protein; AMP1, transgenic plant; linker propeptide; protein expression; plant defensin; RSAPP2; antifungal protein; AFP2.
                                                 Amino acid sequence of a fusion protein of DmAMP1 and RSAFP2
     03-JUL-2000 (first entry)
       EXECUTED TO THE TENT OF THE TE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance of rice paddy against pathogenic microbes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents an antibacterial protein, designated radishin, isolated from Raphanus sativus (radish). A phage or plasmid comprising radishin can be used for increasing resistance of paddy and rice blast disease against pathogenic microbes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 AIGGCIAAGITIGCGICCAICAICGCACTICITITIGCIGCICTIGITCITITIGCIGCT
                                                                                                                                                                                                                                            Raphanus sativus; antibacterial; plant; resistance; paddy; radishin; pathogenic microbe; radish; rice blast disease.
                                                                                                                                                                                             Raphanus sativus antibacterial protein radishin SEQ ID NO:2.
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Mismatches:
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                                              AAY91117 standard; protein; 80 AA.
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97.50%
93.75%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                  Raphanus sativus.
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                                                                                                                                                                                                                                                                                                                                                                 JP2000116379-A.
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                                                                                                AAY91117;
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DB:
RESULT 9
AAY91117
ID AAY91
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The present sequence represents a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (RsAPP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is posttranslationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, v. S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 ITCGAAGCACCAACAATGGTGGAAGCACAQAAGTTGTGCGAAAGGCCAAGTGGGAACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 MetalalysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 AIGGCIAAGTIIGCGICCAICCAICGCACIICIIIIIIGCIGCICIIGIICIIIIIIGCIGCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ray JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     De Bolle MFC, Evans IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
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                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 33; Fig 34; 151pp; English.
                                                                                                                                                                        "DMAMP1"
                                                                                                                                                                                                                                    /note= "linker"
                                                                                                                                                                                                                                                                                                 /note= "RsAFP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Broekaert WF, Francois IEJA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-GB002716.
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98GB-00026753.
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96.25%
95.00%
55.59%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-246564/
N-PSDB; AAZ99339.
Synthetic.
Dahlia merckii.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 187 AA;
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                                                                                                                                                  Protein
                                                                                                                                                                                                        Peptide
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The invention relates to sunflower anti-pathogenic proteins such as pathogenesis-related protein-5 (PR5), defensin and berberine bridge enzyme (BBE). DNA constructs containing nucleotide sequences encoding the anti-pathogenic proteins are useful for increasing resistance against pathogens e.g. fungal pathogen in moncoco or dicot plants. The purified sunflower proteins (PR5, defensin or BBE) and compositions containing the proteins are useful for controlling plant pathogen by using procedures of spraying, dusting, scattering or seed coating, to the plants or the proteins are useful as genetic markers in disease resistance breeding programs. Promoters of environment of the pathogen. The anti-pathogenic genes are useful as genetic markers in disease resistance breeding programs. Promoters capable of driving expression of the proteins are useful to express proteins can also be used in agricultural and pharmaceutical compositions as antifungal and antimicrobial agents. The nucleotide sequences encoding and for enhancing plant defense mechanism. The present sequence

represents a radish antifungal defension (Swiss-Prot Accn No. P30230),
128 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerArgThrTrp 147
                                                                                                                            Increasing pathogen (e.g. fungus, bacteria and virus) resistance in plants, comprises transforming plants with a DNA construct containing a nucleic acid sequence encoding anti-pathogenic proteins.
                                                                                                                                                                                                                                                                                                                                                  Sunflower; anti-pathogenic; pathogenesis-related protein-5; PRS; BBE; defensin; berberine bridge enzyme; plant pathogen; disease resistance; agricultural; pharmaceutical; antifungal; antibacterial; antiviral; antimicrobial; gene therapy; radish.
                                 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
                                                                   148 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla
                                                                                                      196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 4; 86pp; English.
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                                                                                                                                                                                                           AAB61792 standard; protein; 80
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99US-0162904P.
2000US-00589733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-2000; 2000WO-US017090
                                                                                                                                                                                                                                                                                                                Radish antifungal defensin.
                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Raphanus sativus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 80 AA;
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                                                                                                                                                                                                                                              AAB61792;
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Alignment Scores: Pred. No.:

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                                                                                           75
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                                                                                                                                                                                                                                       ArgHisG1ySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An antibacterial protein gene of Wasabia japonica - useful as a food- or
                                                                                                                                TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG
                                                                                                                                                                                          41 SerGlyValCysGlyAsnAsnAsnAsnAlaCysLysSanGlnCysIleArgLeuGluLysAla
                                                                                                       1 MetAlaLysPheAlaSerIleIleValLeuLeuPheValAlaLeuValValPheAlaAla
                                                                                                                                              136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
                                                                                                                                                                                                                       CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                       ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTTTTTGCTGCT
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           Conservative:
Mismatches:
Indels:
Gaps:
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Mismatches:
Indels:
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  Matches:
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Matches:
                                                               US-10-006-252A-19 (1-414) x AAB61792 (1-80)
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                                                                                                                                                                                                                                                                                        AAY57564 standard; protein; 80
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417.00
95.00%
92.50%
55.45%
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96.25%
90.00%
54.12%
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         Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Eutrema wasabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               feed-additive.
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01-MAR-2000
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Pred. No.:
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                                 Query Match:
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136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 TICGAAGCACCAACAAIGGIGGAAGCACAGAAGIIGIGCGAAAAGGCCAAGIGGGACAIGG 135
                                                                                                       61 ArgHisGlySerCysAsnTyrIlePheProTyrHisArgCysIleCysTyrPheProCys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents an Arabidopsis PDF1.2 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
21 PheGluAlaProSerMetValGluAlaGlnLysLeuCysGluLysSerSerGlyThrTrp 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetalaLysPheAlaSerllelleThrLeullePheAlaAlaLeuvalLeupheAlaAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Manners JM;
                                             196 CGACATGGATCTTGCAACTATGTCTTCCCAGGTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 AIGGCIAAGITIIGCGICCAICAICGCACTICTITIIGCIGCICTIGITCTITITIGCIGCI
                                                                                                                                                                                                                                                                                                 Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                            AAW40351 standard; protein; 80 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96GB-00013753.
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403.00
95.00%
88.75%
53.59%
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                                                                                                                                                                                                                                                                   A. thaliana PDF1.2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene from Arabidopsis.
                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
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Best Local Similarity:
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                                                                                                                                                                                                            AAW40351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence represents a Butrema wasabi (Wasabia japonica) gamma-thionin protein from the present
                                                         TTCGAAGCACCACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
                                                                                                                   TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                             CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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                1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheSerAla 20
                                                                          PheGluAlaProSerMetValGluAlaGlnLysLeuCysGluLysSerSerGlyThrTrp 40
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ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                        Wasabia japonica; gamma-thionin; plant; disease-resistant plant.
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Matches:
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                                                                                                                                                                                                                                                                   ABP53725 standard; protein; 80
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 80 AA;
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Query Match:
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           80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the Arabidopsis PDF1.2 protein which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
                                          CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                         Manners JM;
                                                                                                                                                                                                   Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Terras FRG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                      1. .29 //label= signal
30 .80 /label= PPD1.2 /note= "plant defensin"
                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                              Ä.
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                                                                                                           AAW40346 standard; protein; 80
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                                                                                                                                                                              A. thaliana PDF1.2 protein.
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                                                                                                                                                                                                                                    Arabidopsis thaliana.
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N-PSDB; AAV10633.
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16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCT 75

US-10-006-252A-19 (1-414) x AAW40346 (1-80)

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80 71 72 0

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403.00 95.00% 88.75% 53.59%

Best Local Similarity: Query Match: DB:

Percent Similarity:

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                                                                                                                                                              CGACATGGATCTTGCAACTATGTCTTCCCAGCTCAAAGTGTATCTGCTACTTTCCTTGT 255
21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
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                                                                                                                       41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla
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Job time : 62.5 secs
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SOFTWARE: Patentin FC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99042/SEE.36525/US/A
                        US-08-377-687-19

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US-08-971-982-19

US-09-077-951-8

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US-09-077-951-8

US-09-077-951-8

US-09-077-951-8

US-09-077-951-8

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US-09-077-951-69

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US-09-077-951-20

US-09-077-951-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUND P.A.
APPLICANT: CAMMUE, RRUND P.A.
APPLICANT: CAMMUE, RRUND P.A.
APPLICANT: CAMMUE, REDRAY W.B.
APPLICANT: TERRAAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: DERGAS, FRANKY R.G.
ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W.
GTTY: MASHINGTON
STATE: D.G.
CCONTRY: USA
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COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-377-687-49
; Sequence 49, Application US/08377687
; Patent No. 5538525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:

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RESULT 1
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-WODEL-frame+ n2p.mcdel -DEV=xlp
-Q=/cgn2_1/USFTO_spool_p/US10006252/runat_11052004_141658_22839/app_query.fasta_1.583
-Q=/cgn2_1/USFTO_spool_p/US10006252/runat_11052004_141658_22839/app_query.fasta_1.583
-DB=1ssued_Partence_AA_OFWTD=fastan_SUFFIX=rai_AINWATCH=50.1_LOOPCT=60
-LOOPEXT=0 -UNITS=bits_STRAT=1 -Enb=-1 -MATRIX=bloon_TRR_MIN=0 -TRR_MIN=15
-MODE_LOCAL_OTFMTP=pto_NORM=xt -TRR_MIN=0 -TRR_MIN=0 -ALIGN=15
-WODEL=LOCAL_OTFMTP=pto_NORM=xt -LI052004_141658_22839 -MCDU=6 -LOFU=3
-NO_MMAP_LARGEQUERY_NEG_SCGRES=0 -WAIT_DSPBLOCK=100 -LONGLOG
-DEV_TIMEOOT=120 -WARN_TIMEOUT=20 -TRREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-ncapExT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                   Sequence 49,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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                                                                                                                                                             May 11, 2004, 17:00:09 ; Search time 22 Seconds
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1: /cgn2_6/ptOdata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                    OM nucleic - protein search, using frame_plus_n2p model
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US-08-777-192-49
US-09-103-499-20
US-09-829-381D-20
US-09-877-687-59
US-08-377-687-59
US-08-971-982-59
US-08-971-982-59
US-09-589-733C-21
US-09-589-733C-21
US-09-6657-67
US-09-689-733C-21
US-09-689-733C-21
US-08-677-67
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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752
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seq length: 200000000
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Match Length DB
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Maximum DB s
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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BROEKAERT, WILLEM P.
APPLICANT: CAMMUE, BRUND P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERAS, FRANKY R.G.
APPLICANT: TERAS, FRANKY R.G.
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: CUSHMAN DARBY & CUSHMAN: 1100 NEW YORK AVENUE, N.W. WASHINGTON
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APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49, Application US/08777192; Patent No. 5824869; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTER STICS:
LENGTH: 80 amino acids
TYPE: amino acid
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100.00%
100.00%
58.78%
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MOLECULE TYPE: protein
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Best Local Similarity:
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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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REDIUM TYPE: FLORDPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-No. 6187904-1997
CLASSIFICATION: <unimal column of the col
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REGISTRATION NUMBER: 16,773
REPERRICE/DOCKET NUMBER: 99042/SEE.36525/US/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         880000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-006-252A-19 (1-414) x US-08-777-192-49 (1-80)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: BIOCIDAL PROTEINS NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BROEKAERT, WILLEM F. CAMMID, BARINO P.A. OSBORN, RUPERT W. REES, SARAH B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TERRAS, FRANKY R.G. VANDERLEYDEN, JOZEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49, Application US/08971982 Patent No. 6187904 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                 TELEFAX: 202-822-0944
| INFORMATION FOR SEQ ID NO: 45
| SEQUENCE CHARACTERISTICS:
| LENGTH: 80 amino acids
| TYPE: amino acid
| MOLECULE TYPE: protein
| US-08-777-192-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        442.00
100.00%
100.00%
58.78%
                                       TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
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STATE: D.C.
COUNTRY: USA
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DB:
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196 CGACANGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 SerGlyValCysGlyAsnAsnAsnAlaCysLySAsnGlnCysIleAsnLeuGluLySAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTGCTGCT 75
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Sequence 20, Application US/09103489

Patent No. 6215648

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Shah, Yonnie S.

APPLICANT: Rosenberger. Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSES: Charles E. Cohen, Monsanto Company, BB4F

STREET: St. Louis

STATES Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Petentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: P. 10, Version #1.30 APPLICATION NUMBER: US/09/103,489 FILING DATE: 24-UN-1998 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: Cohen, Charles E. REGISTATION NUMBER: 34,565 REFERENCE/DOCKET NUMBER: 34,565 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION 100 ATTORNEY 1314) 537-6224
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-006-252A-19 (1-414) x US-08-971-982-49 (1-80)
                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELECOMMUNICATION INFORMATION:
              TELEPHONE: 202-861-3000
TELEPK: 202-862-0944
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERIFICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                       5.13e-45
442.00
100.00%
100.00%
58.78%
                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonkie S.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for COI TITLE OF INVENTION: Plant Pathogenic Fungi
FILE BETERENCE: 38-21 (10700) C.
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
ENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
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Mismatches:
Indels:
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Mismatches:
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                                                                                                                                                                                                     Length:
Matches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.74e-44
434.00
98.75%
98.75%
57.71%
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98.75%
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57.71%
                                        80 amino acids
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ORGANISM: Raphanus sativus
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                             STRANDEDNESS:
1 TOPOLOGY: linear
1 MOLECULE TYPE: peptide
US-09-103-489-20
                                                          amino acid
                                                                                                                                                                                                                                                               Best Local Similarity:
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Best Local Similarity:
                                                                                                                                                                                                                                            Percent Similarity:
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US-09-829-381D-20
                                                                                                                                                                                  Alignment Scores:
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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135

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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
                                                                                      136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                          196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                               21 PheGluAlaGluThrMetValGluAlaGluLysLeuCysGluArgProSerGlyThrTrp 40
                                                                                                                41 SerGlyValCysGlyAsnAsnAsnAnalaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
                                                                                                                                                                                                    61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: WINDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN DARBY & CUSHWAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      Sequence 59, Application US/08377687
Patent No. 5538525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 aming acids
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98.75%
97.50%
57.58%
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CCUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                   US-08-377-687-59
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1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20

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196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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Mismatches:
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                                                                                                                                                                                                    APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMIE, BRUNO P.A.
APPLICANT: CAMMIE, BRUNO P.A.
APPLICANT: SEES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/ACENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.3
TELEPHONE: 202-61-3000
TELEPHONE: 202-61-3000
TELEPHONE: 202-61-3000
                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                     ; Sequence 59, Application US/08777192; Patent No. 5824869; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
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98.75%
97.50%
57.58%
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MOLECULE TYPE: protein
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C
                                                                                                                                    US-08-777-192-59
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TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG 135

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TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
                                 21 PheGluhlaProThrMetValGluhlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
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                                                                                136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
                                                                                                                  41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla
                                                                                                                                                              196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                                     61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
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                                                                                                                                                                                                                     RESULT 9

US-09-589-733C-21

Sequence 21, Application US/09589733C

Parent No. 6677503

GENERAL INFORMATION:
APPLICANT: Bidney, Dennis L.
APPLICANT: Branch, Dennis L.
APPLICANT: Duvick, Jon
APPLICANT: Duvick, Jon
APPLICANT: Lu, Guihua
ITILE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
ITILE OF INVENTION: Genes and their Uses
FILE REFERENCE: 5718-90
CURRENT FILING DATE: 2000-06-08
PRIOR PILING DATE: 2999-06-23
PRIOR PILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSEQ for Windows Version 3.0

LEAGTH: 80

LANDER DATE: 100 21

LEAGTH: 80

LEAGTH: 80

LEAGTH: 80

LEAGTH: 80

LEAGTH: 80
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Mismatches:
Indels:
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Matches:
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Sequence 23, Application US/09589733C
Patent No. 6677503
GENERAL INFORMATION:
APPLICANT: Bidney, Dennis L.
APPLICANT: Crasta, Oswald R.
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95.00%
92.50%
55.45%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
      92
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41 SerGlyValCysGlyAsnAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
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                                                  TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-No. 6187904-1997
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
RECISTRATION NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                       REES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-08-971-982-59
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                                                                                                                                                                                                      RESULT 8
US-08-971-982-59
; Sequence 59, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEPAX: 202-862-0944
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
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98.75%
97.50%
57.58%
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COUNTRY: USA
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Percent Similarity:
Best Local Similarity:
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Alignment Scores:

Pred. No.:

Query Match: DB:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTATCTTTCCTTGT 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 AFGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT 75
APPLICANT: Duvick, Jon
APPLICANT: Hu, Xu
APPLICANT: Hu, Xu
APPLICANT: Lu, Guinua
TITLE OF INVENTION: Suuflower Anti-Pathogenic Proteins and
TITLE OF INVENTION: Genes and their Uses
FILE REPREMENT: 5718-09
CURRENT APPLICATION NUMBER: US/09/589,733C
CURRENT FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: 60/140,646
PRIOR APPLICATION NUMBER: 60/140,646
PRIOR APPLICATION NUMBER: 60/162,904
PRIOR FILING DATE: 1999-10-1
NUMBER OF SEQ ID NOS: 41
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
SEQ ID NO 23
SEQ ID NO 23
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Sequence 15, Application US/08627706

Sequence 15, Application US/08627706

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Charles E. Cohen, Monsanto Company, BB4F 700 Chesterfield Village Parkway No. 5773696th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEVELORS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
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Matches:
Conservative:
Mismatches:
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Gaps:
                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.38e-39
397.00
92.50%
87.50%
52.79%
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ADDRESSE: Charles E.
STREET: 700 Chesterfie
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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76 TICGAAGCACCAACAATGGTGGAAGCACAGAAGTIGTGCGAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 GluHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTGTTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lidag, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Younie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STARE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-FOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-006-252A-19 (1-414) x US-08-627-706-15 (1-79)
                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                        REFERENCE/DOCKET NUMBER: 38-21(10700) A TELECOMMUNICATION INFORMATION: TELEFONE: (314)537-6224 TELEFONE: (314)537-6047 INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
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APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/09103489 Patent No. 6215048 GENERAL INFORMATION:
                ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                     396.50
96.25$
88.75$
52.73$
                                                                                                                                                                                                                         79 amino acids
                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-627-706-15
                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 63198
                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG 135
                                                                                                                                                                          136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                               196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTAGTTTTCCTTGT 255
                                                     1 MctAlalysPheAlaThrileIleSerLeuleuPheAlaAlaLeuValLeuPheAlaAla 20
                                                                                                                          21 PheGlualaProThrMetValAspala---ArgleuCysGluArgProSerGlyThrTrp 39
                                40 SerGlyValCysGlyAsnAsnAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION DATA:

RAPLICATION NUMBER: US 08/002,480

FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:

MELEPHONE: 202-861.3000

MELEPHONE: 202-861.3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140000
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/08377687

Patent No. 5538525

GENERAL INFORMATION:
APPLICANT: BROEKABET, WILLEM F.
APPLICANT: CANAUE, BRUNO P.A.
APPLICANT: CANAUE, BRUNO P.A.
APPLICANT: CANAUE, SARAH B.
APPLICANT: TEREAS, FRANKY R.G.
APPLICANT: VANNERENCENEN, OOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STRATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.96e-29
309.00
100.00%
100.00%
41.09%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 51 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202-822-0944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3Y: linear
TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
Percent Similarity:
Best Local Similarity:
Query Match:
1
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Pred. No.:
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Sequence 15, Application US/09629381D

Patent No. 6653280

GENERAL INFORMATION

APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yonnie S.

TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi

TITLE OF INVENTION: Plant Pathogenic Fungi

TITLE OF INVENTION: Plant Pathogenic Fungi

CURRENT FILING DATE: 2001-04-09

PRIOR PAPLICATION NUMBER: US/09/829,381D

PRIOR PAPLICATION NUMBER: 09/103,489

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20

SOCTWARE: Patentin version 3.1

LENGTH: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 TICGAAGCACCAACAAIGGIGGAAGCACAGAAGIIGIGGGAAAAGGCCAAGIGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 CGACATGGATCTTGCAACTATGTCTTCCCAGGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 SerGlyValCysGlyAsnAsnAsnAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 GludisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 79
                                                                                                                                                                                                                                                                                                                                                                                                                                       16 ATGGCTAAGITTGCGTCCATCATCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                172
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION NUMBER: 34,565
REPERBENCH/COCKTA NUMBER: 38-21 (10700) A
TELECOMMINICATION INFORMATION:
TELEPAN: (314) 537-624
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                1.58e-39
396.50
96.25%
88.75%
52.73%
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396.50
96.25%
88.75%
52.73%
                                                                                                                            LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity: 8
Query Match:
DB:
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ORGANISM: Alyssum Sp.
US-09-829-381D-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-829-381D-15
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Pred. No.:
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103 CAGAAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCA 162
                                                                                           163 TGCAAGAATGAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 TGCAAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTC 222
                                                21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Stah, Dilip M.
APPLICANT: Win Younde S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STRET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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Matches:
Conservative:
Mismatches:
US-10-006-252A-19 (1-414) x US-08-377-687-19 (1-51)
                                                                                                                                                       223 CCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-006-252A-19 (1-414) x US-08-627-706-18 (1-51)
                                                                                                                                                                      41 ProAlaHisLysCysIleCysTyrPheProCys 51
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; Sequence 18, Application US/08627706
; Patent No. 5773696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.96e-29
309.00
100.00$
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41.09$
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63198
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DB:
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Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
Qy 223 CCAGCTCACAAGTGTATCTGCTTGT 255
Db 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Search completed: May 11, 2004, 17:06:19
Job time: 27 secs
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Sequence 49, Appl sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 15, Appl Sequence 14, Appl Sequence 15, Appl Sequence 15, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 18, Appl Sequence 22, Appl Sequence 34, Appl Sequence 34, Appl Sequence 31, Appl Sequence 56, Appl Sequence 51, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Sequence 6
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Sequence
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                                                                                                                                                                                                                                                         US-09-759-584-19
US-09-732-181-18
US-09-732-181-18
US-10-881-391A-18
US-10-388-361A-34
US-10-006-252A-28
US-10-0072-809A-35
US-10-0072-809A-35
US-10-0072-809A-35
US-10-0072-809A-35
US-10-0072-809A-35
US-10-006-252A-58
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US-10-006-252A-79
US-10-006-252A-79
US-10-006-252A-79
US-10-006-252A-79
US-10-006-252A-79
US-10-006-252A-79
9 US-09-759-584-49

9 US-09-829-381A-20

12 US-08-9-731A-20

9 US-09-759-584-59

12 US-10-636-396-11

9 US-09-732-561-14

12 US-10-636-396-13

13 US-10-636-396-13

14 US-10-636-396-13

15 US-09-732-561-14

16 US-09-732-561-14

17 US-09-732-561-19

18 US-09-732-381A-19

19 US-09-732-561-19

10 US-09-732-561-19

10 US-09-732-561-19

11 US-10-066-252A-59

12 US-10-066-252A-59

13 US-10-066-252A-59

14 US-10-066-252A-59

15 US-10-066-252A-59

16 US-10-066-252A-61

17 US-10-066-252A-61

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19 US-10-066-252A-61

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19 US-10-066-19

19 US-10-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BROBEABRT, WILLEM F.
APPLICANT: CAMMUB, BRUNO P.A.
APPLICANT: OSBOSN, RUDBET W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 49, Application US/09759584; Patent No. US20010014732A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
  20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-09-759-584-49
    мы менен ме
                                                                                                                                                                       Command line parameters:
-MODEL=frame+ n2p model - DEV=xlp
-MODEL=frame+ n2p model - DEV=xlp
-MODEL=frame+ n2p model - DEV=xlp
-DS=VD11shed_spool p/US10006252/runat_11052004_141659_22867/app_query.fasta_1.583
-DB=PUD11shed_applications_AA - QFWT=fastan - SUFFIX=rapb - WINMATCH=0.1
-LOOPELST - LOOPELST - UNITE=bits - START=1 - END=-1 - WATRIX=blosum62
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR XMX=0.1
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR XMX=0
-THR_XIN=0 - ALIGN=15 - NODE=LOCAL - OUTFWT=pct - NORM=ext - HEARSIZE=500 - MINLEN=0
-MAXLEN=20000000000 - USER=USL006552 @CGN 1 1.13 @runat 11052004 141659 22867
-NCPU-6 - ICPU-3 - NO MMAP - LARGEQUERY - NG $\overline{S}$ GCRES=0 - NATT - DSPBLOCK=100
-LONGICG - DEV_TINEOUT=120 - WARN TIMEOUT=30 - THERADS=1 - XGAPDP=10 - XGAPDFXT=0.5
-FGAROOP=6 - FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
                                                                                                                                                   May 11, 2004, 17:02:19 ; Search time 41.5 Seconds (without alignments) 5537.958 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                        - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1140673 seqs, 277566755 residues
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Query Score Match Length DB

Minimum DB seq length: 0 Maximum DB seq length: 200000000

0.5 7.0 7.0

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

Searched:

BLOSUM62

Scoring table:

US-10-006-252A-19 752

Perfect score:

Title:

Sequence:

nucleic

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Run on:

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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGAAGTGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTTGCTGCT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetAlaLysPheAlaSerIleIleAlaLeuDeuPheAlaAlaLeuVheAlaAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 PheGluhlaProThrMetValGluhlaGlnLysLeuCysGluhrgProSerGlyThrTrp 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCys1leCysTyrPheProCys 80
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ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Wosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              000000
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759.584
                                                                                                                                                                                                                                                99042/SEE.36525/US/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
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Matches:
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                                             ALLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/ABENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/f
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Sequence 20, Application US/09829381A

Setent No. US20020144306A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      TELEPHONE: 202-861-3000
TELEPAX: 202-861-3000
INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS: LENGTH: 80 amino acids
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100.00%
100.00%
58.78%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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Best Local Similarity:
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DB:
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Sosenberger, Clindy A.
TITLE OF INVENTION: Plant Pathogenic Fungi
FITLE OF INVENTION: Plant Pathogenic Fungi
FITLE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US/99/829,381D
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR PILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGAATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 SerGlyvalCysGlyAsnAsnAshAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCys1leCysTyrPheProCys 80
                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNEY/AGENT INFORMATION:
NAME: COREN, Charles E.

REGISTRATION NUMBER: 34,565

TELECOMUNICATION INDER: 38-21 (10700)A

TELECHONE: (314) 537-6047
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0 0 1 0 0
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Conservative:
Mismatches:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
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; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-829-381A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/10681972; Publication No. US20040064850A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 20;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score: 434.00
Percent Similarity: 98.75%
Best Local Similarity: 98.75%
Query Match: 57.71%
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US-10-681-972-20
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MOLECULE TYPE:
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DB:
                                                                                Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                              1 MetalalygphealaSerileileAlaLeuLeuPheAlaalaLeuValLeuPheAlaala 20
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                                                                                                                                                                                                                                                                                                                                                                                                         41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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                                                                            0 0 0 0 0
                                                                          Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                  US-10-006-252A-19 (1-414) x US-10-681-972-20 (1-80)
                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUB, BRUNO P.A.
APPLICANT: OSBORN, RUBERT W.
APPLICANT: SEES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTONNEY AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/S
TELECOMUNICATION INFORMATION:
TELEFRANE: 202-861-3000
FILEFRANION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 59, Application US/09759584 Patent No. US20010014732A1 GENERAL INFORMATION:
                                                                      6.28e-41
434.00
98.75$
98.75$
; ORGANISM: Raphanus sativus
US-10-681-972-20
                                                                                                                            Best Local Similarity:
                                                                                                         Percent Similarity:
                                                       Alignment Scores:
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US-09-759-584-59
                                                                                                                                         Query Match:
DB:
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136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
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Sequence 21, Application US/10636396

Publication No. US20040073971A1

GENERAL INFORMATION:
APPLICANT: Bidney, Dennis L.
APPLICANT: Crasts, Oswald R.
APPLICANT: Duvick, Jon
APPLICANT: Lu, Guihua
ITILE OF INVENTION: Genes and their Uses
FILE REPERBNCE: 5718-90
CURRENT FILING DATE: 2003-08-07
PRIOR PILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/140,646
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENDER: DATE: 
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0 4 4 0 0
   Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                Gaps:
8.18e-41
433.00
98.75%
97.50%
57.58%
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417.00
95.00%
92.50%
55.45%
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US-10-636-396-21
                                                                      Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
DB:
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136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                              196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTTTTCCTTGT 255
21 PheGlugluProThrMetValGluAlaGlnLySLeuCysGlnArgProSerGlyThrTrp 40
                                                                                       41 SerGlyValCysGlyAsnAsnAsnAsnAsnCysLysAsnGlnCysIleArgLeuGluLysAla 60
                                                                                                                                                                  61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
                                                                                                                                                                               Sequence 16, Application US/09732561

Sequence 16, Application US/09732561

Sequence 16, Application US/09732561

SENERAL INFORMATION:
APPLICANT: Terras, Franky
APPLICANT: Pernainckx, Iris
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Razan, Kemal
APPLICANT: Razan, Kemal
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: ZENECP >---
STREET:
STREET:
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTATION VUNBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMUNICATION INFORMATION:
TELEPHONE: 302) 886-1699
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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US-10-006-252A-19 (1-414) x US-09-732-561-16 (1-80)

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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                                                                                                            196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
16 AIGGCIAAGITIGCGICCAICAICGCACTICITITIGCIGCICTIGITCITITITGCIGCT 75
                           21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
                                                                                                                                                                                                       41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
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COMPUTER READBLE FORM:

REDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: LEW PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/732,561

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/202,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis PDF1.2 amino acid sequence
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Thomma, Bart
APPLICANT: Terras, Franky
APPLICANT: Perninckx, Iris
APPLICANT: Perninckx, Iris
APPLICANT: Manners, John
APPLICANT: Kazan, Kemal
APPLICANT: Brockaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMONICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: (0 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-UW-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09732561
Patent No. US20020035738A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: ZENECA Ag Products: 1800 Concord Pike Wilmington
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STATE: DE
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Score: Percent Similarity Best Local Similar Query Match: DB: US-10-006-252A-19 QY 16 ATGGG Db 1 MetA.	imilarity 1 Similas
Best Local Query Matc DB: US-10-006- QY Db	l Simila
DB: US-10-006- QY Db	. 50
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RESULT 9 US-10-636-396-23	.396-23
Sequence	23, Apj
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APPLICA ; APPLICA	NT: Bld
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TITLE	F INVENT
CURRENT ;	APPLICE
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SEQ ID NO 23	0 23
; LENGTH: 8 ; TYPE: PRT	: 80 PRT
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Pred. No.:	scores:
Score: Percent Sir	milarit
Best Local Similari Query Match:	Similar
US-10-006-3	052A-19
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ò	76 TTCGAA
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PAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG 135
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                                                                                                          SCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTTTTTTGCTGCT
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  Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                        (1-414) \times US-09-732-561-14 (1-80)
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                                                                                                                                                                                                                                                                                                                                                                                                     CATION NUMBER: US/10/636,396
G DATE: 2003-08-07
TION NUMBER: US/09/589,733C
DATE: 2000-06-08
DATE: 1999-06-23
TION NUMBER: 60/162,904
TION NUMBER: 60/162,904
DATE: 1999-11-01
ID NOS: 41
tSEQ for Windows Version 3.0
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US20040073971A1
ION:
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vick, Jon
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; ORGANISM: Alyssum Sp.
US-10-681-972-15
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Best Local Similarity:
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US-10-681-972-15
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US-09-759-584-19
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LENGIH: 79
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136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
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               61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                              nu, increases Cindy A. Rosenberger, Cindy A. Rosenberger Cindy A. TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION SUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
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Matches:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                             Sequence 15, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 79 amino acids
                                                                                                                                                                                                                                  APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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Best Local Similarity:
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DB:
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Sequence 15, Application US/10681972

Publication No. US20040064850A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: W. Yonnie S.
APPLICANT: W. Younie S.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
                                                                                                            196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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                              40 SerGlyValCysGlyAsnAsnAsnAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
                                                                                                                                           60 GluHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 79
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Mismatches:
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APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/09759584;
Patent No. US20010014732A1
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUR, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
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88.75%
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US-09-829-381A-18
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Pred. No.:
                                                                    COUNTRY:
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            STREET:
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                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                 99042/SEE.36525/US/A
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Terras, Franky
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Kazan, Kemal
APPLICANT: Broekaert, Willem
ITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SI
TELECHONNICATION INFORMATION:
TELECHONE. 202-861-3000
TELEFAX: 202-822-994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/09732561 Patent No. US20020035738A1 GENERAL INFORMATION:
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100.00%
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TYPE: amino acid
STRANDEDNESS: single
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ADDRESSEE: ZENECA AG
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Best Local Similarity:
Query Match:
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STATE: D
COUNTRY:
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US-09-732-561-19
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TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0000
                                                      ZIP: 19850
COMPUTER READABLE FORM:
Maddin Type: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                          PILING DATE:

CLASSIFICATION:

PRIOR APPLICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/202,638

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/202,638

FILING DATE: 20-70N-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hohenschutz, Liza D.

REGISTRATION NUMBER: 33,712

REFERENCE/DOCKET NUMBER: 33,712

REFERENCE/DOCKET NUMBER: 39055/US:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
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Patent No. US20020144306A1

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip M.
Wu, Yonnie S.
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IMMEDIATE SOURCE:
CLONE: Rs-AFP1
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Wilmington
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Best Local Similarity:
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Sequence 18, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALVAFP from Alyssum and Methods for Control FILLE REFERENCE: 39-21 (1070), C
FILLE REFERENCE: 39-21 (1070), C
CURRENT APPLICATION NUMBER: US/0), C
CURRENT FILING DAIE: 2003-10-09
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700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                              COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                        CURRENT APPLICATION DATA

APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION CURREN: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: COREN, Charles E.
REPERENCE/DOCKEY NUMBER: 38-21 (10700) A
TELECOMMUNICATION INFORMATION:
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Matches:
Conservative:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-829-381A-18
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PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (314) 537-6224
TELEPAX: (314) 537-6224
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.28e-26
309.00
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                                                                            ZIP: 63198
COMPUTER READABLE FORM:
                CITY: St. Louis
STATE: Missouri
                                                                                                                           MEDIUM TYPE:
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Best Local Similarity:
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US-10-681-972-18
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103 CAGAAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCA 162
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Mismatches:
Indels:
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Job time : 42.5 secs
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 51
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$66220
$28990
$57809
T14866
$23574
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S11156
T06766
T02667
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S66218
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T06599
C84433
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TO6381
JC7897
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 May 11, 2004, 16:59:19 ; Search time 18.5 Seconds (without alignments) 4305.221 Million cell updates/sec
                                                                                                                                                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                - protein search, using frame_plus_n2p model
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Tilliugal protein I precursor - radish
C;Species: Raphanus sativus (radish)
C;Species: Raphanus sativus
C;Accession: Tillio; A42842
R;Persas F. R; Eggermont, K; Kovalewa, V; Raikhel, N.V.; Osborn, R.W.; Kester, A. Plant Cell 7, 568-573, 1955
A;Pitle: Small cysteine-rich antifungal proteins from radish: their role in host def. A;Reference number: Z16976
A;Reference number: Z16976
A;Reference number: Z16976
A;Rocession: Tillio
A;Roleoule type: RRBL:U18557; NID:g644773; PID:g609322
A;Residues: 1-80 <TER
A;Reference: EmBL:U18557; NID:g644773; PID:g609322
A;Residues: 1-80 <TER
A;Reference: EmBL:U18537; NID:g644773; PID:g609322
A;Residues: Gf. von novel classes of plant antifungal proteins from radish (Rapi A;Recession: A4284
A;Reference number: A42842; MUID:92348373; PMID:L639777
A;Residues: 30-73 <TE2>
A;Residues: Seed
A;Rote: sequence extracted from NCBI backbone (NCBIP:109570)
A;Gene: ARPI
C;Function:
A;Gene: ARPI
C;Function: A;Gene: ARPI
C;Function: A;Gene: ARPI
C;Function: A;Gene: ARPI
C;Function: A;Gene: ARPI
C;Function: A;Gene: ARPI
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C;Gene: ARPI
C;Function: A;Gene: ARPI
C;Gene: ARPI F;1-29/Domain: signal sequence #status predicted <SIG>F;30-80/Product: antifungal protein 1 #status predicted <MAT>

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB

Length

Query Match

Result Š. 80

Length:

1.8e-39

Alignment Scores: Pred. No.:

Antifungal protein hypothetical prote antifungal protein antifungal protein defensin AMPI - Da

antifungal protein antifungal protein probable antifunga

T10183 T02621 T02621 T02622 T96622 T10291 T10291 T10291 G86328 G86328 S28998 S28988 S28988

protein T4012.7

antifungal protein antifungal protein antifungal protein probable antifunga probable antifunga

Description

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21 PheGluGluProThrMetValGluAlaGluLysLeuCysGlnArgProSerGlyThrTrp 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: gamma-thionin
C;Keywords: antifungal
F;1.29-Domain: signal sequence #status predicted <SIG>
F;30-80/Product: antifungal protein 4 #status predicted <MAT>
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A,Molecule type: DNA
A,Residues: 1-80 <ROU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Description: has antifungal activity
C;Superfamily: gamma-thionin
F;l-43/Domain: signal sequence #status predicted <SIG>
F;44-80/Product: antifungal protein 2 #status predicted <MAT>
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Note: sequence extracted from NCBI backbone (NCBIP:109572)
C;Genetics:
C;Function:
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probable antifungal protein T19L18.17 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear oress)
C;Species: Arabidopsis thaliana (mouse-ear oress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
C;Datesion: T02621; E846555
R;Rounaley, S.D.; Kaul, S.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, Ssubmitted to the EMBL Data Library, August 1998
A;Pescription: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
A;Reference number: Z14681
A;Accession: T02621
                                                                                                196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
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R/Terras, Fx.; Goderis, I.J.; Penninckx, I.J.; Osborn, R.W.; Broekaert, W.F.
submitted to the EMBL Data Library, April 1996

A.Reference number: 216981

A.Reference number: 216981

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Residues: preliminary; translated from GB/EMBL/DDBJ

A.Residues: 1-80

A.Residues: 1-80

A.Cross-references: EMBL: 897318

A.Experimental source: cultivar Ronde Rode Kleine Witpunt
C.Genetics:
                                                                                                                                                                                                                                                                                                                                      antifungal protein 4 precursor – radish
C,Species: Raphanus sativus (radish)
C,Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
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protein T4012.7 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Parabidopsis thaliana (mouse-ear cress)
C;Accession: F96787
R;Theologis, A.; Ecker, U.R.; Palm, C.U.; Federspiel, N.A.; Kaul, S.; White, O.; Alon ansen, N.F.; Hughes, B.; Huizar, L.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Yi, Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallc A;Ttile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: R86141; MUID:21016719; PMID:11130712
A;Seatus: preliminary
A;Molecule type: DNA
A;Restine: Dread DNA
A;Restine: Conditionary
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C;Genetics:
A;Gene: T4012.7
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88.75%
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397.00
92.50%
87.50%
52.79%
                         A,Gene: At2g26010, T19L18.18
A,Map position: 2
A,Introns: 22/1
C,Superfamily: gamma-thionin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Map position: 1
C,Superfamily: gamma-thionin
                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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A,Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413721
A,Experimental source: cultivar Columbia
R,Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Gronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A,Reference number: A84420; MUD:20083487; PMID:10617197
A,Rocession: B84655
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-80 csTO
A,Cross-references: GB:AE002093; NID:g3413721; PIDN:AAC31244.1; GSPDB:GN00139
A,Genetics:
C,Genetics:
A,Map position: 2
A,Introns: 22/1
C;Superfamily: gamma-thionin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probable antifungal protein T19L18.18 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T02622; D84655
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
A;Reference number: Z14681
A;Reference number: Z14681
A;Reference number: T08622
A;Status: translated from GB/EMBL/DDBJ
A;Reference number: Los GROUS
A;Status: Lranslated from GB/EMBL/DDBJ
A;Residues: LSO
A;Rouls 1.80
A;Rouls 1.80
A;Rouls 2.7; Rounsley, S.D.; Shee, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
A;Ross-references: EMBL:ACO04747; NID:93413696; PID:93413711
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shee, T.P.; Benito, M.I.; Trown, C.D.; Fujii, C.Y.;
A;Ross-references: EMBL:ACO04747; NID:93413711
A;Experimental source: cultivar Columbia
R;Lin, X.; Raul, S.; Rounsley, S.D.; Shee, T.P.; Benito, M.I.; Trown, C.D.; Fujii, C.Y.;
A;E.D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.A;Accession: D84655
A;Status: preliminary
A;Accession: D84655
A;Accession: D84655
A;Cross-references: GB:AE002093; NID:93413711; PIDN:AAC31234.1; GSPDB:GN00139
C;Genetics:
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
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F;1-29/Domain: signal sequence #status predicted <8IG>P;30-79/Product: antifungal protein 3 #status predicted <MAT>
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C;Superfamily: gamma-thionin
                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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A; Molecule type: DNA
A; Residues: 1-80 <STO>
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antifungal protein 3 precursor - radish
c;Species: Raphanus sativus (radish)
c;Date: 16-Uul-1899 #sequence_revision 16-Uul-1899 #text_change 20-Uun-2000
C;Accession: T10243
K;Terras, F.R.G.; Goderis, I.J.; Penninckx, I.J.; Osborn, R.W.; Broekaert, W.P.
submitted to the EMBL Data Library, April 1896
A;Accession: T10243
A;Accession: T10243
A;Accession: T10243
A;Molecule type: mRNA
A;Residues: 1-79 <TER>
                                                                                  TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                     196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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21 LeuGluAlaProMetValValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
                                                                                                                                 41 SerdiyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
                                                                                                                                                                                                                   ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: Z16214
A;Accession: T07917
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-79 < SOH>
A;Cross_references: EMBL:US9459; NID:g1399229; PIDN:AAB03224.1; PID:g1399230
                                                                                                                                                                                                                                                                                                                                 antifungal protein - rape
Cispecies: Brassica napus (rape)
Cibate: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jun-2000
CiAccession: T07917
Rischn, U.; Lee, C.M.; Lee, M.H.; Kim, J.H.
submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCT
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A;Experimental source: cultivar Ronde Rode Kleine Witpunt
C;Genetics:
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Matches:
Conservative:
Mismatches:
Indels:
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C.Superfamily: gamma-thionin
C.Keywords: antifungal
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Theologis A.; Ecker, V.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Comm, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Maure 406, 816, 820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, R.; Rondey, D.; Sawanc, H.
A.Authors: Salzberg, S.L.; Schwarz, J.R.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Reference and analysis of chromosome 1 of the plant Arabidopsis.

A.Reference mumber: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                               76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGAACATGG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: AE005173; NID: 99857525; PIDN: AAG00880.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable antifungal protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
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                                 Conservative:
Mismatches:
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      Matches:
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67.90%
49.38%
27.53%
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antifungal protein 1 - Arabidopsis thaliana (fragment)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 25-Peb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
C.Accession: S28995
B.Terras, F.R.G.: Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Camn FEBS Lett. 316, 233-240, 1993
A.Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicac A.Reference number: S28989; WUID:93138130; PMID:8422949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C)Accession: S20989
R)Terras, F.R.G; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cam FBES Lett. 316, 233-240, 1993
A)Tille: A new family of basic cysteine-rich plant antifungal proteins from Brassica A;Feference number: S20909; MUID:93138130; PMID:0422949
A;Molecule type: protein
A;Residues: 1-27 <TERS
C;Superfamily: gamma-thionin
                                                                                                                                                                                                                                                                                                                                                                                                                   166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACGACGATCTTGCAACTATGTCTTCCCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 CAGAAGTIGIGCGAAAGGCCAAGIGGGACAIGGICAGGAGICTGIGGAAACAATAACGCA 162
                                                                                                                                                                                                                                                                                                106 AAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 165
                                                                                                                                                                                                                                                                                                                                                      56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antifungal protein 1 - turnip (fragment)
C;Species: Brassica rapa (turnip)
C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
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Mismatches:
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Mismatches:
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                         Length:
Matches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 GCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                                                                                       US-10-006-252A-19 (1-414) x G86328 (1-56)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-006-252A-19 (1-414) x S28989 (1-27)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 TGCAAGAATCAGTGCATTAAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 CysLysAsnGlnCyslleAsn 27
                   2.31e-09
164.00
64.00$
50.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.24e-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 1-27 <TER>
                                                                                        Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
   Alignment Scores:
Pred. No.:
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C;Species; Arabidopsis thaliana (mouse-ear cress)
C;Species; Arabidopsis thaliana (mouse-ear cress)
C;Accession: G86328
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 1816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwarzz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUD:21016719; PMID:11130712
A;Rocession: G86328
A;Residues: 1-56 <STO>
A;Residues: 1-50 <STO
A;Residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C. Accession: S28991, S28992 Cammue, R. Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, R. Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, R. Tels Lett. 316, 233-240, 1993
A. Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae A. Reference number: S28999; MuID:93138130; PMID:8422949
A. Reference number: S28999; MuID:93138130; PMID:8422949
A. Residues: 1-30 cTER>
A. A. Residues: 1-30 cTER>
A. A. Residues: 1-30 cTER>
A. Residues: 1-33 cTE2>
C. Superfamily: gamma-thionin
136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                               196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAG---TGTATCTGCTACTTTCCT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 CAGAAGTTGTGCGAAAGGCCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCA 162
                                                                                                                                                     1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAla 20
                                                     40 SerGiyArgCysValAsnAspTyrGlnCysArgAspHisCysileAsnAsnAspArgGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: AE005172; NID: 99795584; PIDN: AAF98402.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Brassica napus (rape)
C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 CysLysAsnGlnCysIleAsnLeuGluLys 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-006-252A-19 (1-414) x S28991 (1-30)
                                                                                                                                                                                                                                                                                                                                                                                                            antifungal protein 1 - rape (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.58e-10
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100.00%
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23.27%
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                          80 Cys 80
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A;Map position: 1
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Score: 156.00 Matches: 26 Percent Similarity: 100.00% Conservative: 1 Best Local Similarity: 96.30% Mismatches: 0 Query Match: 20.74% Indels: 0	rity: 100.00% 20.08% 2
328995 (1-27)	US-IU-UU0-ZSZR-IF (I-414) X SZ8595 (I-25) QY 103 CAGAAGTIGTGGGAAAGGGCGAAGTGGGA
Oy 103 CAGAAGTTGTGCGAAAGGCCAAGTGGGAGTCAGGAGTCTGTGGAAACAATAACGCA 162	
Oy 163 TGCAAGAATCAGTGCATTAAC 183	21 CysLysAsnGlnCys 25
RESULT 14 S6621 defensin AMP1 - Dahlia merckii defensin AMP1 - Dahlia merckii N,Alternate names: seed antifungal protein C;Species: Dahlia merckii C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999 C;Accession: S66221 R;Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Leuven FBS Lett. 368, 257-262, 1995 A;Title: Isolation and characterisation of plant defensins from seeds of Asteraceae, Fak A;Reference number: S66218; WUID:95354848; PMID:7628617 A;Accession: S66221 A;Accession: S66221 A;Accession: S66221 C;Keywords: antifungal	Search completed: May 11, 2004, 17:05:18 Job time: 19.5 secs
Alignment Scores: 2.82e-08 Length: 50 Pred. No.: 154.00 Matches: 26 Score: 62.00\$ Conservative: 5 Bercent Similarity: 52.00\$ Mismatches: 19 Query Match: 20.48\$ Indels: 0 BB:	
US-10-006-252A-19 (1-414) x S66221 (1-50)	
Oy 106 AAGTIGTGCGAAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGC 165	
Oy 166 AAGAATCAGTGATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTTCCCA 225	
Qy 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255 Db 41 LysHisMetCysPheCysTyrPheAsnCys 50	
RESULT 15 228993 antifungal protein 1 - white mustard (fragment) C;Species: Sinapis alba (white mustard) C;Species: Sinapis alba (white mustard) C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000 C;Accession: S28993 R;Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, FEBS Lett. 316, 233-240, 1993 A;Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae A;Reference number: S289893 A;Accession: S28993 A;Accession: S28993 A;Accession: Drotein A;Residues: 1-25 <ter> C;Superfamily: gamma-thionin</ter>	
Alignment Scores: 6.39e-08 Length: 25 Pred. No.: 151.00 Matches: 25 Percent Similarity: 100.00\$ Conservative: 0	

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Mismatches:
Indels:
Gaps:
                  x S28993 (1-25)
                                          3TGC 177
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nCys 25
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Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Minimum DB seq Maximum DB seq

Searched:

142 137 131.5 114

Score

Result

Database :

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vigna ungui
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mus musculu
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arabidopsis
capsicum an
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P78990 kluyveromyc
Q90y54 brachydanio
                                                                                                                                                arabidopsis
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mus musculu
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                                                                                                                                                                                                                                                                                                    caenorhabdi
                                                                                                                                                                  drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=R.sativus; STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed; MEDLINE=95299350; PubMed=7780308; Terras F.R.G., Eggermont K., Kovaleva V., Raikhel N.V., Osborn R.W., Kester A., Rees S.B., Torrens S., Van Leuven F., Vanderleyden J., Cammue B.D.A., Broekaert W.F.; "Small cysteine-rich antifungal proteins from radish: their role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus (Rape), and Raphanus sativus (Radish).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids, eurosids II, Brassicales; Brassicace, Brassica.

NCBI_TaxID=3708, 3726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W., anderleyden J., Cammue B.P.A., Broekeert W.F.; "A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae species."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 30-73.
SPECIESER. satisfus; IISSUE-Seed;
MEDLINE-92348373; PubMed=1659777;
Terras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F.,
Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
"Analysis of two novel classes of plant antifungal proteins from radish (Raphanus sativus L.) seeds.",
           092ul8 8
0118646 v
011783 F
001708 7
000001708 7
0000017 8
0000017 8
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P35556 Y
P18168 C
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Q8cg19
P20346
                                                                                                                                                                                                                                Q07008
P81930
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFPI_BRANA STANDARD; PRT; 80 AA. P3025; 04163; 00.1-APR-1903 Rel. 25, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cysteine-rich antifungal protein 1 precursor (AFP1).
                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                               NTC1 RAT
PSD2 PEA
LTBS MOUSE
LTBL MOUSE
                                                                                                                                 PSDI PEA
THG2 ARATH
DL DROME
                                                                                                                                                                DL DROME
LEM3 RAT
DEF2 SPIOL
THGF HELAN
ASF2 HELAN
DEFL CAPAN
10KD VIGUN
DR39 PEA
D230 PEA
AD02 MOUSE
THG3 ARATH
THG1 ARATH
DEF2 CAPAN
AX2_BETVU
                                                                                                                                                                                                                                                                                      P322_SOLTU
L112_CAEEL
FBN2_HUMAN
SERR_DROME
                                                                                                                                                                                                                                                                                                                                                     JAG3_BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=B.napus; TISSUE=Seed;
MEDLINE=93138130; PubMed=8422949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEBS Lett. 316:233-240(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Cell 7:568-573(1995).
SEQUENCE FROM N.A.
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 RESULT
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-02=Cqqq21_1/02pC grool p/USIQ0066252/runat_11052004_141657_22786/app_query.fasta_1.583
-02=Cqqq21_1/02pC grool p/USIQ0066252/runat_11052004_141657_22786/app_query.fasta_1.583
-001175=bits -02parta_1 - ENT=1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-0001761GN=500 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 - ALIGE=15 - MODE=LOCAL
-0017FMT=pct - NORM=sxt - HEAPSIZE=500 - MINIX=0 - MAXIEN=200000000
-0017FMT=pct - NORM=sxt - HEAPSIZE=500 - MINIX=0 - MAXIEN=200000000
-0017FMT=pct - NORM=sxt - HEAPSIZE=500 - MINIX=0 - MAXIEN=200000000
-0017FMT=pct - NORM=sxt - HEAPSIZE=500 - MINIX=0 - MAXIEN=200000000
-0017FMT=pct - NORM=sxt - HEAPSIZE=500 - MINIX - DSPBLOCK=100 - LONGLOG - ICPU=3
-NORM - LARGEQUERY - NORG SCORES=0 - MAIT - DSPBLOCK=100 - LONGLOG - FGAPPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELBEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 024331 raphanus sa
09f123 arabidopsis
080994 arabidopsis
080995 arabidopsis
080995 arabidopsis
039313 raphanus sa
024332 raphanus sa
193021 sinapis alb
193022 inapis alb
193022 hassica ra
192257 heisanus
193028 brassica ra
193028 brassica na
024115 nicotiana p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P30225 brassica na
P30230 raphanus sa
                                                                                                         (without alignments)
3079,578 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                          1 gttttattagtgatcatggc......
                                                                                             ; Search time 14 Seconds
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

    protein search, using frame_plus_n2p model

                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                      141681 segs, 52070155 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
                                                                                             May 11, 2004, 16:57:50
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AFP1
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length: 2000000000
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Match Length DB
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40.3
31.1
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eurosids II; Brassicales; Brassicaceae; Raphanus
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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                     76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 SerGlyValCysGlyAsnAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids,
J. Biol. Chem. 267:15301-15309(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYSTEINE-RICH ANTIFUNGAL PROTEIN 1.
PYRROLIBOUR CARBOXYLIC ACID.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CBS SIMILARITY.
CSB90FAAC8DA6C2B CRC64;
                                                             -!- SUBUNIT: Forms oligomers in its native state.
-!- SUBCRLIULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 2 precursor (APP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PP01014, Cana-thionin, 1.
ProDom, PD002594, G Brothionin, 1.
SMART, SM00505, Knotl, 1.
PROSITE, PS00940; GAMMA THIONIN, 1.
Plant defense, Fungicide; Signal; Multigene family, Pyrrolidone carboxylic acid.
SIGNAL
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P30231; 1AYJ.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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PIR; T10176; T10176.
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8734 MW;
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Best Local Similarity:
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Pred. No.:
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ID AFP2_RAPSA
ID AFP2_RAPSA
DT 01-APR
DT 01-APR
DT 28-FEB
DT CN-CT
CN AFP2.
OS Raphan
OC Eukary
OC Sperma
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                           Terras F.R.G., Eggermont K., Kovaleva V., Raikhel N.V., Osborn R.W., Kester A., Rees S.B., Torrekens S., van Leuven F., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
"Small cysteine-rich antifungal proteins from radish: their role in host defense."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                    TISSUE=Seed;
MEDINE=22348373; PubMed=1639777;
Terras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F.,
Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
"Analysis of two novel classes of plant antifungal proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYSTEINE-RICH ANTIFUNGAL PROTEIN 2. PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
746110D9A8CE6370 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probom, PD002594; G_Purothionin; 1.
SWART; SW00505; Knockli, 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
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                                                    SEQUENCE FROM N.A.
STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
MEDLINE=95299350; PubMed=7780308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          radish (Raphanus sativus L.) seeds."
J. Biol. Chem. 267:15301-15309(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, F30231, 1AYJ.
InterPro; IPR00811'6, Gamma-thionin.
InterPro; IPR003614; Knot1.
Pfam; PP00304; Gamma-thionin; 1.

    -!- SUBCELLULAR LOCATION: Secreted.

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417.00
95.00%
92.50%
55.45%
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                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 30-65.
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NCBI_TaxID=3726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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RAPSA

RAPSA

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                                                                                                                                                                                     TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                               196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
              1 MetAlaLysPheValSerIleIleThrLeuLeuPheValAlaLeuValLeuPheAlaAla 20
                                                                                                                                                                                                                                                                                                                                   ArgHisGlySerCysAsnTyrIlePheProTyrHisArgCysIleCysTyrPheProCys 80
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                                                                       TTCGAAGCACCAACAATGGTGGAAGCACAGAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG
                                                                                                                      21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgSerSerGlyThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Columbia;
MEDLINE=99397451; PubMed=10470850;
MEDLINE=99397451; PubMed=10470850;
Mispainma N., Tabata S.; Nakamura Y., Asamizu E., Kotani H.,
Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 5. IX.
Sequence features of the regions of 1,011,550 bp covered by seventeen PI and TAC clones.";
                                                                                                                                                                                                                                          41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            core eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vanoosthuyse V., Miege C., Dumas C., Cock J.M.;
Submitted (JUN-2000) to Swiss-Prot.
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9FIZ3; P82786;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cysteine-rich antifungal protein LCR77 precursor (AFP).
LCR77 OR AT5G44420 OR MFC16.8
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cations (By similarity).
--- SUBCELLULAR LOCATION: Secreted (By similarity).
--- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta, Magnoliophyta, eudicotyledons, core en
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00940; GAMMA THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
Pyrrolidone carboxylic acid.
29 POTENTIAL.
CHAIN 30 80 PROBABLE CYSTEINE-RICH
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InterPro; IPR003614; Knot1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00304; Gamma-thionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB017065; BAB09149.1; -. HSSP; P30231; 1AYJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 6:183-195(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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NCBI_TaxID=3702;
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                                                                                         CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
80
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                                                                                                                               61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raphanus sativus (Radish).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Raphanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: Possesses antifungal activity sensitive to inorganic cations (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-cv. Ronde Rode Kleine Witpunt; TISSUE-Seed;
Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Broekaert W.F.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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16-0cT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 4 precursor (APP4).
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Mismatches:
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HSSP; P30231; 1AYJ.
InterPro; 1PR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
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405.00
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MEDLINE-20083487; PubNed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul C., Rounsley S.D., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiolantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Spermatophyta; Massolicales; Brasslcaceae; Arabidopsis.
NCPL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-DCT-2003 (Rel. 41, Last annotation update)
Probable cysteine-rich antifungal protein At2g26020 precursor (AFP).
AT2G26020 OR 19118.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
  BY SIMILARITY.
2D0DAFB38E3B6321 CRC64;
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                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                    Gaps:
   76
8518 MW;
                                            1.54e-36
403.00
95.00%
88.75%
53.59%
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   54
80 AA;
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SEQUENCE FROM N.A.
                                                                                Similarity:
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                                   Alignment Scores:
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EMBL; AC004747; AAC31244.1; -. PIR; T02621; T02621.

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TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cysteine-rich antifungal protein At2g26010 precursor (AFP).
AT2G26010 OR T1918.18.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; wagnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
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STRAIN=cv Columbia;
STRAIN=cv Columbia;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Town T.J., Aban M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                 PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
81B106058BAFFCC7 CRC64;
                   Prant, Products, August, Products, Products, Products, Products, General-Chionin; 1.
SMART; SM005594; Generalin; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
Product defense; Pungicide; Signal; Multigene family; Pyrrolidone carboxylic acid.
SIGNAL 1.
29 PROBABLE CYSTEINE-RICH
CHAIN 30 80 PROBABLE CYSTEINE-RICH
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InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
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93.75%
87.50%
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Best Local Similarity:
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SEQUENCE
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No
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Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cations.
                                                                                                                                                     Raynal M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thaliana.";
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EMBL;
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                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
PROBABLE CYSTEINB-RICH ANTIFUNGAL PROTEIN
ATACS610.
PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetAlaLysSerAlaAlaIleIleThrPheLeuPheAlaAlaLeuValLeuPheAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    930224; Q42179; Created)
01-APR-1993 (Rel. 25, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
Cysteine-rich antifungal protein 1 precursor (AFP1) (Anther-specific protein S18 homolog).
AFP1 OR PDF1.1 OR ATIG75830 OR T4012.6 OR T4012.7.
 Nature 402:761-768(1999).
                                       SUBCELLULAR LOCATION: Secreted (By similarity). SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                 PROSITE; PS00940; GAMMA THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                           99E1E0D4443AD67B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                80
71
71
0
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-006-252A-19 (1-414) x AFP2_ARATH (1-80)
                                                                                                                                                                                          HSSP, P30231; 1AVJ.
InterPro; IRR008176; Gamma-thionin.
InterPro; IRR00814; Knotin.
Pfam; PF00304; Gamma-thionin, 1.
ProDom; PD002594; GPurothionin, 1.
SMART; SM00055; Knoti; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                   EMBL; AC004747; AAC31234.1; -.
                            cations (By similarity).
                                                                                                                                                                                                                                                                                                                                                            80
65
74
76
8580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           4.27e-36
399.00
93.75%
88.75%
53.06%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                     29
80
                                                                                                                                                                                  T02622; T02622.
                                                                                                                                                                                                                                                                                                                                                           33
44
50
54
80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity:
                                                                                                                                                                                                                                                                                                               30
                                                                                                                                                                                                                                                                                                                                     30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
DISULFID
SEQUENCE
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APP1 AR
ID AF
DT O1
DT 15
DT 28
DE CY
DE CY
GN AF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Theologis A., Ecker U.R., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Abhite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fulia C.Y., Addith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L., Hunter J.L., Jonkins J., Johnson-Hopson C., Khan A., Lam B., Hunter J.L., Jonkins J., Johnson-Hopson C., Khan A., Lia B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Milischer J., Miranda M., Nguyen N. Nierman W.C., Osborne B.I., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Venter J.C., Davis R.W.; Raser C.M., Venter J.C., Davis R.W.; Raser C.M., Venter J.C., Davis R.W.; Paralisa B., Hallshish B., Marshidopsis
Eukaryoča, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W., Vanderleyden J., Cammue B.P.A., Broekaert W.F., Brantly of basic cysteine-rich plant antifungal proteins from Brassicaceae species.", FEBS Lett. 316:233-240(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99178804; PubMed=10080719;
Williams R.W., Clark S.E., Meyercwitz E.M.;
Genetic and physical characterization of a region of Arabidopsis chromosome 1 containing the ChayATA1 gene.";
Plant Mol. Biol. 39:171-176(1999).
                                                                                                                                                                                                                                                                                                                                     ..
Σ
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                                                                                                                                                                                                                          SEQUENCE FROW N.A.
STRAIN=cv. Columbia,
Yaral M., Grellef F., Laudie M., Meyer Y., Cooke R., De
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: Forms oligomers in its native state.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-cv. Columbia; TISSUE-Seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Seed;
MEDLINE=93138130; PubMed=8422949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z27258; CAA81770.1; -.
EMBL; Z29957; CAA82845.1; -.
EMBL; X91916; CAA63009.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 408:816-820(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TICGAAGCACCAACAAIGGIGGAAGCACAGAAGIIGIGCGAAAGGCCAAGIGGAAAIGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCys1leAsnLeuGluLysAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetalalysSeralaThrilevalThrleuPhePheAlaAlaLeuValPhePheAlaAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LeuGluAlaProMetValValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 AIGGCTAAGTTIGCGTCCATCATCGCACTTCTTTIGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
peprantophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicacee; Brassica.
NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Naehan;
Sohn U., Lee C.M., Lee M.H., Kim J.H.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                               CYSTEINE-RICH ANTIFUNGAL PROT)
PYRROLIGONE CARBOXYLIC ACID.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
C -> F (IN REF. 1).
           HSSP; P30231; 1AVJ.
InterPro; 1PR008176; Gamma-thionin.
InterPro; 1PR008176; Gamma-thionin.
InterPro; 1PR008174; Knocl.
InterPro; PR00304; Gamma-thionin; 1.
Prom; P00304; Gamma-thionin; 1.
SMART; SM00505; Knocl.; 1.
PROSITE: P500940; GAMMA_THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family; Pytrolidone carboxylic acid.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                            C -> F (IN REF. 1).
99F34A8DA360441F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i6-OCT-2001 (Rel. 40, Created)

i6-OCT-2001 (Rel. 40, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Cysteine-rich antifungal protein 3 precursor (AFP3).
                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 AA.
                                                                                                                                                                                                                                                                                                                                       Matches:
                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-006-252A-19 (1-414) x AFP1_ARATH (1-80)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                   80
80
65
74
76
33
8709 MW;
                                                                                                                                                                                                                                                                                                                       7.11e-36
                                                                                                                                                                                                                                                                                                                                    397.00
92.50%
87.50%
52.79%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus (Rape)
 PIR; F96787; F96787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     Similarity:
                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFP3 BRANA
Q39313;
                                                                                                                                                                                MOD_RES
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                           DISULFID
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                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                     Best Local
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CCCCCC RANGERACE COCCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGAACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 GlnHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 AIGGCIAAGTTIGCGICCAICAICGCACTTCTTITIGCTGCTCTTGTICTTTTTGCTGCT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 PheGluAlaProThrMetValGluAla---LysLeuCysGluArgSerSerGlyThrTrp 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raphanus sativus (Radish).

Rubaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Raphanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYSTEINE-RICH ANTIFUNGAL PROTEIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Broekaert W.F.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cations (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                           PER; 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.71, 10.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
3B5289FCFEA48936 CRC64;
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16-0CT-2001 (Rel. 40, Last sequence update)
18-0CT-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 3 precursor (AFP3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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BY SIMILARITY
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                                                                                                                                                   EMBL; U59459; AAB03224.1; -.
PIR; T07917; T07917.
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79
64
73
75
8555 MW;
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394.50
93.75%
91.25%
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DISULFID
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SEQUENCE
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AFP3_RAPSA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetAlaLysPheAlaSerIleValAlaLeuLeuPheAlaAlaLeuValValPheAlaAla
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-203 (Rel. 44, Last annotation update)
28-FBB-203 (Rel. 44, Last annotation update)
Cysteine-rich antifungal protein I (AFP) (ML)
Sinapis alba (White mustard) (Brassica hita).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids, NCBI_TAXID=3728,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96433791; PubMed=8836771;
Neumann G.M., Condron R., Polya G.M.;
"Purification and mass spectrometry-based sequencing of yellow mustard (Sinapis alba L.) 6 kDa proteins. Identification as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYSTEINE-RICH ANTIFUNGAL PROTEIN :

BY SIMILARITY.

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BY SIMILARITY.
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PIR; T10243; T10243.
HSSP, P30231; 1AVJ.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR008176; Gamma-thionin.
Prom; P600304; Gamma-thionin; 1.
ProDom; P0002594; G Purcthionin; 1.
PROSITE; P800940; GAMMA_THIONIN; 1.
PROSITE; P800940; GAMMA_THIONIN; 1.
PLANT defense; Fungicide; Signal; Multigene family.
SIGNAL
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Matches:
Conservative:
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393.50
95.00%
90.00%
52.33%
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8479 MW;
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443
53
AA;
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TISSUE=Seed;
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APPL SINAL
L PAPPL SINAL
DT 01-APR
DT 28-FRB
DT 02-APR
DT 28-FRB
DT 02-APR
DT 02-APR
DT 02-APR
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222
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                                                                                                                                                                    STRUCTURE BY NMR.
MEDLINE=98300344; PubMed=5636715;
MEDLINE=98300344; PubMed=5636715;
Fant F., Vranken W.F., Broekaert W.F., Borremans F.A.M.;
"Determination of the threadmensional solution structure of Raphanus sativus antifungal protein 1 by 1H NMR.";
J. Mol. Biol. 279:257-270(1998)
-I. FUNCTION: Possesses antifungal activity sensitive to inorganic
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                                                                                                                                                                                                                                                                                                                                                                 INCEPTED, INCOMENTAL . ALCONOMIN 1.
Prodom; PD002594; G Purothionin; 1.
SWART; SW00505; Knocl; 1.
PROSTINE; PS00940; GAMAA THIONIN; 1.
Plant defense; Fungicide; 3D-structure; Pyrrolidone carboxylic acid.
MOD RES. 1. PYRROLIDONE CARBOXYLIC ACID.
                                                                              Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W., Vanderleyden J., Cammue B.P.A., Broekaert W.F.; "A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae species.";
                                                                                                                                                                                                                                                                      cations.
-!-SUBUNIT: Forms oligomers in its native state.
-!-MASS SPECTROMETRY: MW-5677; MW_ERR=1.0; METHOD=Electrospray.
-!-SIMILARITY: Belongs to the plant defensin family.
PDB: 1AVJ; 28-JAN-98.
InterPro; IPR008176; Gamma-thionin.
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Mismatches:
Indels:
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-rich antifungal protein 2A (APP2A) (M2 Sinapis alba (White mustard) (Brassica hitta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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antifungal proteins.";
Int. J. Pept. Protein Res. 47:437-446(1996)
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                                                                   MEDLINE=93138130; PubMed=8422949;
                                                                                                                                            FEBS Lett. 316:233-240(1993).
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309.00
100.00%
100.00%
41.09%
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45
47
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Best Local Similarity:
                                           1-25.
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                                        SEQUENCE OF
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AF2A_SINAL
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DB:
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AF2A_SINAL
ID AF2A
AC P3023
DT 01-AF
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DE CYSTE
OS SINAE
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103 CAGAAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCA 162
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Sinapis.
                                                                                                                                                                                                                                                               MEDLINE 593138130; PubMed=8422949;
PETRARS F. NG., TOTREKENS S., Van Leuven F., Osborn R.W.,
Vanderleyden J., Cammue B.P.A., Broekaart W.F.;
"A new family of basic cysteine-rich plant antifungal proteins from
Basslaceaes species.";
FEBS Lett. 316:233-24(11993).
-! - FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Forms oligomers in its native state.
-!- MASS SPECTROMETRY: WW-5705; WW ERR-0.8; METHOD=Electrospray.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                MEDLINE=56433791; PubMed=8836771;
Neumann G.M., Condron R., Polya G.M.;
"Purification and mass spectrometry-based sequencing of yellow
mustard (Sinapis alba L.) 6 KDa proteins. Identification as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00505; KnoTl; 1.

PROSITE; PS00940; GAMMA THIONIN; 1.

Fungicide; Phosphorylation; Pyrrolidone carboxylic acid.

MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.

MOD_RES PHOSPHORYLATION (BY CDPK).

DISULRID 4 51 BY SIMILARITY.
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 2B (AFP2B) (M2B).
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 ProAlaHisLysCyslleCysTyrPheProCys 51
                                                                                                                                                                                                    Int. J. Pept. Protein Res. 47:437-446(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-006-252A-19 (1-414) x AF2A_SINAL (1-51)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P30231; 1AVJ.
InterPro; IPRO08176; Gamma-thionin.
InterPro; IPR008176; Gamma-thionin.
Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.73e-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303.00
100.00%
96.08%
40.29%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36
45
45
                                                                                                                                                                                        antifungal proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 AA;
                                                                                                                                                                                                                   [2]
SEQUENCE OF 1-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                        TISSUE=Seed;
                                                                                                                                                                                                                                                                                                                                                                                   cations.
                                                                                                                                                                                                                                                    TISSUE=Seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                      SEQUENCE
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ID AF2B_SIN

AC 010989;

DT 01-0CT-11

DT 28-FBB-21

DE CYSteine
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160 GCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTC 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 AlaCysArgAsnPheCysIleLysLeuGluLysSerArgHisGlySerCysAsnIlePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Sinapis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 28, Last sequence update)
01-REB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteine-rich antifungal protein 1 (APP1) (Fragment).
Brassica rapa (Turnip).
Rukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBL TaxID=51350;
                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00940; GAMMA THIONIN; FALSE NEG.
Fungicide; Pyrrolidone Carboxylic acid.
MOD RES
                                                                                                       TISSUE=Seed,
MEDLINE=96433791; PubMed=8836771;
Neumann G.M., Condron R., Polya G.M.,
Neumann G.M., condron R., Polya G.M.,
"Purification and mass spectrometry-based sequencing of yellow
mustard (Sinapis alba L.) 6 kba proteins. Identification as
mustard (Sinapis alba L.) 6 kba proteins. Identification as
Intifungal proteins.,
Int. J. Pept. Protein Res. 47:437-446(1996).
-i- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                                                                                                                                                     -!- SUBUNIT: Forms oligomers in its native state.
-!- MASS SPECTROMETRY: WW-5840; WW_ERR=1.2; METHOD=Electrospray.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
A060FCBC13A8D1FB CRC64;
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20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 PheProSerAsnLysCysIleCysTyrPheProCys 52
Sinapis alba (White mustard) (Brassica hirta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                 HSSP, P30231, 1AYJ.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                                                                               Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G Purothionin; 1.
SMART; SM00505; Knot1; 1.
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TISSUE-Seed;
MEDLINE-93138130; PubMed-8422949;
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84.62%
76.92%
31.05%
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37
46
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Best Local Similarity:
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P30227;
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DISULFID
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                                                                                             SECUENCE
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us-10-006-252a-19.rsp

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 CAGAAGTIGIGCGAAAGGCCAAGIGGGACAIGGICAGGAGICIGIGGAACAAIAACGCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-1994 (Rel. 29, Last annotation update)
Anther-specific protein STHB precursor (Fragment).
Helianthus annuus (Common sunflower).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant Mol. Biol. 15.643.646(1990).
-!- FUNCTION: Anther-specific cell wall protein which could contribute
    to the cell wall architecture of epidermal anther cells via
    intermolecular disulfide bridges.
-!- TISSUE SPECIFICITY: Epidermal anther cells.
-!- DEVELOPMENTAL STAGE: Late developmental stages.
-!- SIMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=cv. HA401B / Cargill; TISSUE=Anther;
MEDLINE=9133702; Pubmed=2102380;
Domon C., Evrard J.-L., Herdenberger F., Pillay'D.T.N., Steinmetz A.;
"Nucleotide sequence of two anther-specific cDNAs from sunflower
(Helianthus annus L.).";
Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W., Vanderleyden J., Cammue B.P.A., Broekaert W.F., Family of basic cysteine-rich plant antifungal proteins from Brassicaceae species. "
FEBS Lett. 316:233-240(1993).
- !- FUNCTION: Possesses antifungal activity sensitive to inorganic
                                                                                                                             -!- SUBUNIT:
-- SIMILARITY: Belongs to the plant defensin family.
-!- SIMILARITY: Belongs to the plant defensin family.
-!- SIMILARITY: Belongs to the plant defensin family.
HSSP, P30231; 1AVJ.
INTER-PRO; 1R00816; Gamma-thionin.
Pfam; PF00304; Gamma-thionin; 1.
PRODOM; P5002594; Gamma-thionin; 1.
PROSITE; P500940; GAMMa-Thionin; 1.
PROSITE; P500940; GAMMa-Thionin; 1.
Plant defense; Fungicide; Pyrrolidone carboxylic acid.
MOD_RES
                                                                                                                                                                                                                                                                                                                                                 4C85BD9C611D4A9E CRC64;
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 TGCAAGAATCAGTGCATTAAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 CysLysAsnGlnCysIleAsn 27
                                                                                                                                                                                                                                                                                                        161.00
100.00%
100.00%
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Best Local Similarity:
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                                                                                                                       cations.
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HELAN
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106 AAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 165
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36 AsplysArgCys1leAspTrpGluGlyAlaLysHisGlyAlaCysHisGlnArgGluAla 55
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MEDIUSBESSES

MEDIUSBESSION

MEDIUSBESSION

Texras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,

Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,

Vanderleyden J., Cammue B.P.A., Broekeert W.F.;

A. new family of basic cysteine-rich plant antifungal proteins from

Brassicaceae species.",

FEBS Lett. 316:233-240(1993).

-: FEMS Lett. 316:233-240(1993).

-: FEMS Lett. 316:233-240(1993).

-: FEMS Lett. 316:233-240(1993).

-: SUNOTION: Possesses some antifungal activity against B.megaterium.

-: SUBUNIT: Forms oligomers in its native state.

-: SUMILARITY: Belongs to the plant defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
NCBI_TaxID=51350;
                                                                                                                                                                                                                                                                                                                                                                                            ANTHER-SPECIFIC PROTEIN SF18.
GAMMA-THIONIN LIKE DOMAIN.
PROLINE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; 27A9CF4633ADA02B CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Cysteine-rich antifungal protein 2 (AFP2) (Fragment).
Brassica rapa (Turnip).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
23
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 LyshisMetCysPheCysTyrPheAspCys 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-006-252A-19 (1-414) x ASF1_HELAN (1-161)
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         ProDom, PD002594, G Purothionin, 1. SMART; SM05055, Knotl; 1. SM0501E; PS00940, GANWA_THIONIN; 1. Signal; Cell wall. 1. 1. NON, TER.
                                                                                                           HSSP, P30231, 1AYJ.
InterPro, IPR008176, Gamma-thionin.
InterPro, IPR003614, Knotl.
Pfam; PP00304; Gamma-thionin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15363 MW;
                                                        EMBL; X53375; CAA37455.1; -. PIR; S12246; S12246.
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149.00
64.00%
46.00%
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161
161
65
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59
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HSSP; P30231; 1AYJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 AA;
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SIGNAL
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AFP2_BRARA
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InterPro; IPR008176; Gamma-thionin.
ProDom; PD002594; G Purothionin; 1.
PROSITE, PS00940; GAMMA_THIONIN; 1.
PROSITE, PS00940; GAMMA_THIONIN; 1.
PLAN défense; Fungicide; Antibiotic; Pyrrolidone carboxylic acid.
WOD RES
1 PYRROLIDONE CARBOXYLIC ACID.
NON TER 27 27
SEQÜENCE 27 AA; 2891 MW; 571E6D9C611D4A9E CRC64;
                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                    1.07e-07
142.00
96.15%
96.15%
18.88%
                                                                                                                                                    Percent Similarity:
Best Local Similarity: 9
Query Match:
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US-10-006-252A-19 (1-414) x AFP2_BRARA (1-27)

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163 TGCAAGAATCAGTGCATT 180

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21 CysLysAsnGlnCysIle 26

Search completed: May 11, 2004, 17:03:07 Job time: 29 secs

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Q9fs38 eutrema was Q9fs38 eutrema was Q9fk% Drassica ra Q9fk% Drassica ra Q9fx31 arabidopsis Q9fx27 arabidopsis Q9fx27 arabidopsis Q9fx27 arabidopsis Q9fx2 picea ables Q8dx12 picea ables Q4072 picea ables Q4073 picea ables Q94812 pyrus pyrif Q94812 pyrus pyrif Q94812 pyrus pyrif Q94814 pyrus qarbidopsis Q24225 oryza satioopsis Q9500 arabidopsis Q24225 arabidopsis Q24225 arabidopsis Q24225 arabidopsis Q9500 arabidopsis Q9600 caenorhabdi Q39807 glycine max Q81638 triticum ae Q8600 prome sativ Q81638 triticum ar Q81638 prassicum artiv Q81638 prassi
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Q810h2 mus musculu
Q9nap6 caenorhabdi
Q94az8 arabidopsis
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094IN7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Defensin precursor.
Defensin precursor.
Brassica oleracea (Cauliflower).
Brassica oleracea (Cauliflower).
Brassica oleracea (Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids; NCBL_TAXID=3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Esnault R.;
"Brassica oleracea def gene for defensin.";
"Brassica oleracea def gene for defensin.";
submitred (APR-2001) the EMBL/GenBank/DDBJ databases.
EMBL; AJ311046; CAG37558.1;
GO; GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
ProDom; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
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                                                                                                          May 11, 2004, 16:58:28 ; Search time 41 Seconds
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                         protein search, using frame_plus_n2p model
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Maximum Match 100%
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2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Signal.

S H K E S

Pred. No.:

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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG 135
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                                                             ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Brassica.

NCBL_TAXID=51351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Ryang S.-Y., Park Y.-S., Cho T.-J.; Ryang S.-H., Chung S.-Y., Park Y.-S., Cho T.-J.; "Characterization of Chinese cabbage genes induced by Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          syringae pv. tomato...'
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS28180; AAN23105.1; -..
GO; GO: 0003793; F. Gefense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR008176; Gamma-thionin.
Fram; PF00304; Gamma-thionin, 1.
Prodom; PD00559; G Purchionin; 1.
Prodom; PD00559; Knot1; 1.
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80 AA; 8864 MW; 485CC5A95905E92C CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches:
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                                  US-10-006-252A-19 (1-414) x Q9FS38
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MEDITINE=1071227; PubMed=11204773;
Saitoh H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;
Saitoh H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;
Saitoh H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;
Production of antimicrobal defensin in Nicotiana benthamiana with a potato virus X vector.";
Mol. Plant Wicrobe Interact. 14:111-115(2001).
HNSP: P30231; 1AVJ.
GO, GO:0003793; Fidefense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Eutrema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CF2F10ADD38FC87A CRC64;
                                                                      980477DFBD8D2690 CRC64;
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SWART; SM00505; Knotl; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
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          SMART; SM00505; Knotl; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
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80 AA;
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ArgHisGlySerCysAsnTyrValPheProTyrHisArgCysIleCysTyrPheProCys 80
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Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99397451; PubMed=10470850; Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H., Miyalima N., Tabata S.; Structural analysis of Arabidopsis thaliana chromosome 5. IX. Sequence features of the regions of 1,011,550 bp covered by sevent Pl and TAC clones."
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative antifungal protein (Cysteine-rich antifungal protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein activity; IEA.
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PROSITE; PS00940; GAMMA_THIONIN; 1.
SEQUENCE 80 AA; 8550 MW; 44Elf6D8452AC76E CRC64;
                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
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T24C10.12 OR F14C21.57.
Arabidopsis thaliana (Mouse-ear cress).
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InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
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Pfam; PF00304; Gamma-thionin; 1.
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EMBL; AB017065; BAB09150.1; -.
HSSP; P30231; 1AYJ.
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WHITE O', Alons O', Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

White O', Alons O', Chen H., Cheuk R.F., Chin C.W.,

WESCUENCE B., Chan L., Conway A.B., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,

A Dunn P., Etgu P., Feldhlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Dunn P., Etgu P., Feldhlyum T.V., Feng J.-D., Khaykin B.,

A Gill J.B., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A Hunter J.L., Venkins J., Johnson-Hopson C., Khan S., Khaykin B.,

A Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Lin X., Liu S.X., Liu Z.A., Luros G.S., Maiti R., Marziali A.,

A Lin X., Liu S.X., Liu Z.A., Luros G.S., Maiti R., Marziali A.,

A Lin X., Liu S.X., Mayen M., Nguyen M., Neoney T., Rowley D.,

Sakano H., Zalzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wh. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135
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-unaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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| SerGiyargCysValAsnAspTyrGlnCysArgAspHisCysIleAsnAspArgGly
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                                                                                                                                                                                    Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knot1.
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9139 MW; BEFBF4ACA7974071 CRC64;
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PD002594; G_ru
-^<: Knot1
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PIR; F96591; F96591.
HSSP; P30231; 1AYJ.
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                                                                                                   Q9FWR6
                                                            RESULT 7
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                                                                                 O9FWR6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 ACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 GGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :::||||
3 SerSerTyrThrLeuMetLeuPheLeuCysLeuSerIlePheLeuIleAlaSerThrGlu 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 MetMetAlaValGluGlyArgIleCysGluArgArgSerLysThrTrpThrGlyPheCys 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 GCGTCCATCATCGACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCTTTTCGAAGCACCA 87
                                                                                                                                                                                                                                                                                                                                                                                                             Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Theologis A.,
                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Full Length cDNA of gene At1g19610 (GI:15223595)."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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                                                                                                                                                                  Created)
                                                                                                                                                             01-WAR-2002 (TrEMBLrel. 20, Cres
01-WAR-2002 (TrEMBLrel. 20, Last
01-0CT-2003 (TrEMBLrel. 25, Last
Putative defensin AMPI protein.
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181.00
53.95%
40.79%
24.07%
                                                                                                                            PRELIMINARY;
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253 TGT 255
                                        80 Cys 80
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106 AAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEQUENCE FROM N.A.

RA Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buthler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Buehler E., Chao Q., Chin C., Chin C., Choi E., Gonzalez A., La Monrg B., Johnson-Hoppson C., Khan S., Kim C., Koo T., Lee J.M., Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Suhmiter (SEP-2000) to the EMBL/GenBank/DDBJ databases.

REMBL, ACC24609; AAF98402.1; -.

RIF, G86328; G86328.

RIF, G86328; G86328.

RIF, G86328; G86328.

RIF, G86328; Gamma-thionin.

ROS, GO:0003793; F:defense/immunity protein activity; IEA.

RITER-PRO; IPRO08176; Gamma-thionin.

RIF CRODOM; PD002594; G-Purothionin; 1.

RODOM; PD002594; G-Purothionin; 1.

RODOM; PD002594; G-Purothionin; 1.

RODOM; PD002694; G-Purothionin; 1.

RODOM; PG00940; GamMa-THIONIN; 1.

RODOM; ROSSITE; RODE!: AND THIONIN; 1.

RODOM; ROSSITE; RADE!: 1.

REQUENCE 56 AA; 6403 MW; 3BD56EAA25EBC442 CRC64;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
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                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                    208 IGCAACTATGTCCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
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01-0CT-2002 (TrEMBLrel, 22, Last sequence update)
01-0CT-2003 (TrEMBLrel, 25, Last annotation update)
                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyPheAlaCysPheCysTyrPheAsnCys 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
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164.00
64.00%
50.00%
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                                                                                                                                                                                                                                                                                                                                       F14P1.6 protein.
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NCBI TaxID=4220;
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                                                                SEQUENCE
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No.:
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Q84ZX5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 AGTIGIGCGAAAGGCCAAGIGGGACAIGGICAGGAGICIGIGGAAACAAIAACGCAIGCA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 --LeucysGluLysAlaSerGlnThrTrpSerGlyThrCysGlyLysThrLysHisCysA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lycopersicon esculentum (Tomato).
Bukaryota, Viridiplantae, Streeptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 AGAATCAGTGCATTAAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAG
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C STRAIN-WITH.

MEDLINE-95375233; PubMed=7647301;

Milligan S.B., Gasser C.S.;

"Nature and regulation of pistil-expressed genes in tomato.";

I "Nature and regulation of pistil-expressed genes in tomato.";

I Plant Mol. Biol. 28.691-711(1995).

R EMBL; U20591; AAA80496.1; -..

R PIR; S57809; S57809.

R OG, GO:0003793; F:defense/immunity protein activity; IEA.

R InterPro; IPR003614; Knott.

R InterPro; IPR00364; Gamma-thionin.

R Pfem; PF00304; Gamma-thionin; 1.

R SMART; SM00505; Knotl; 1.

S SMART; SM00505; Knotl; 1.
                                                                                      Hu X., Bidney D., Duvick J., Yalpani N., Crasta O., Folkerts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-12003 (TrEMBLrel. 25, Last annotation update)
Flower-specific gamma-thionin-like protein/acidic protein
                                                                                                                         "Oxalate oxidase confers Sclerotinia resistance.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF364865, AAM27941.;
GO; GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR008614; Knott.
Prodom; PP00304; Gamma-thionin; 1.
                                                                                                                                                                                                                                                                                                                    SM00505, Knot1; 1.
SE 108 AA; 11866 MW; 631ECD8F02F21AD0 CRC64;
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33
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Query Match:
                     NCBI_TaxID=4232;
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  Helianthus
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TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annocation update)
Major pollen allergen Art v | precursor |
Artemisia vulgaris (Mugwort).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicocyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Asteroideae; Anthemideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 ThrGlyGlyHisCysSerLysLeu-----GlnArgLysCysLeuCysThrLysProCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 ProdlyLeuCysPheMetAspSerSerCysArgLysTyrCysIleLys---GluLysPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Himly M., Jahn-Schmid B., Dedic A., Kelemen P., Wopfner N., Altmann F., van Ree R., Briza P., Richter K., Ebner C., Ferreira F.; Altmann F., van Ree R., Briza P., Richter K., Ebner C., Ferreira F.; Art V., the major allergen of mugwort pollen, is a modular glycoprotein with a defensin-like and a hydroxyproline-rich domain."; FASEB J. 17:106-108(2003).

EMBL; AF433943; AAO24900.1; -...
GO; GO:0003793; F:defense/immunity protein activity; IEA.

InterPro; IPR008147; Gamma-thionin.
                                                                                                                                                                                                                                                                                                                                                        ATGCCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAJOR POLLEN ALLERGEN ART V 1.
745249C89919F316 CRC64;
POTENTIAL.
GAMMA-THIONIN-LIKE PROTEIN.
ACIDIC PROTEIN.
ADC987ECB620E814 CRC64;
                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                         US-10-006-252A-19 (1-414) x Q40128 (1-105)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Pollen;
MEDLINE=22409970; PubMed=12475905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF00304; Gamma-thionin; 1. SWART; SMO0505; Knot1; 1.
                                                                    11914 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13404 MW;
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139.50
50.00%
                                                                                                                                         8.48e-08
                                                                                                                                                             141.50
58.54%
37.80%
18.82%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
  26
73
105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
25
132 AA;
  1
27 ,
74 1
105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 TAATTT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 ValPhe 75
                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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99

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76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 ProGlyIleCysIleThrLysProProCysArgLysAlaCysIleSer---GluLysPhe 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAD1.

Nicotiana alata (Winged tobacco) (Persian tobacco).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetalaArgSerLeuCysPheMetAlaPheAlaIleLeuAlaMetMetLeuPheValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lay F.T., Schirra H.J., Scanlon M.J., Anderson M.A., Craik D.J.;
Lay F.T., Schirra H.J., Scanlon M.J., Anderson M.A., Craik D.J.;
The three-dimensional solution structure of NaDl, a new floral
defensin from Nicotiana alata and its application to a homology model
of the crop defense protein alfAFP.";
J. Mol. Biol. 0.0-0 (10003).
EMBL, AFSO956; AAN70999.1;
GO; GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR00814; Gamma-thionin.
Pfo0304; Gamma-thionin; 1.
                                                          48 AlaSerArgAshAsnCysLysAshValCys---GlnThrGluGlyPheProSerGlySer
148 GGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCT
                                                                                                                                                                        TGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLOWER-SPECIFIC DEFENSIN.
DA7F41736CEE6AC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105
27
17
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Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                               105
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                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probom; PD002594; G Purchionin; 1. SMART; SM00505; Knotl; 1. PROSITE; PS00940; GAMMA_THIONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lower-specific defensin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN 26 72 F
SEQUENCE 105 AA; 11722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        23,
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53.66%
32.93%
15.43%
                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                       RESULT 12
Q8GTM0
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ID Q4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 TGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAA 192
                                                                                                                                                                                                                                                                                                                               73 GCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAG---------234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 ATGGTGGAAGCACAG---AAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGT 147
                                                                                                                                                                                                   16 ATGGCTAAGTTTGCGTCCATCATC---GCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCT 72
                                                                                                                                                                                                                                                                                                                                                                                         21 GluMetGluAla-----AlaGlySerLySLeuCySGluLySThrSerLySThr 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 TyrserdlyLysCys---AspAsnLysLysCysAspLysLysCysIleGluTrpGluLys 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HisbysArgGluAlaGlyLysGlu 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 TCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCTTTTCGAAGCACCAACA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerArgLeuSerAlaLeuPheLeuLeuValLeuLeuValIleSerIleGlyMetMetGln 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The putative gymnosperm plant defensin (SPII) accumulates after seed germination and a related SPIIB CDNA is found in needles."; Submitted (SEP-202) to the EMBL/GenBank/DDBJ databases.

GO, GO:0003793; F:defense/immunity protein activity; IEA.

InterPro; IPR003176; Gamma-thionin.

Pfam; PR00314; Gamma-thionin, 1.

ProDom; PD002594; G Purcthionin; 1.

ProDom; PD002594; G Purcthionin; 1.

PROSITE; PS00940; GaMMA-THIONIN; 1.

SEQUENCE 83 AA; 8888 MW; E45EF9E61B9AA3D2 CRC64;
                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putarive plant defensin SPIIB.
Picea abies (Norway spruce) (Picea excelsa).
Bukaryota, Viridiplantee, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Coniferales; Pinaceae; Picea.
          139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223283
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Mismatches:
Indels:
      Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 AA.
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Matches:
                                                                    Gaps:
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                                                                                                                                     US-10-006-252A-19 (1-414) x Q84ZX5 (1-132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-006-252A-19 (1-414) x Q8GTL2 (1-83)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||:::||||||::|||
||AlaGlnHisGlyAlaCys-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.14e-05
118.00
51.32%
34.21%
      38.64%
18.55%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 TCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCTTTCGAAGCACCAACA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicctiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 ATGGTGGAAGCACAG---AAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGT
                                                                                                                                        Sharma P., Linneborg A.; Isolation of a cDNA encoding a gamma-thionin-lisolation and characterization of a cDNA encoding a gamma-thionin-like protein from roots of Norway spruce."; Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
BME1, X91487; CAA62761.1; -...
PIR: 714866; 714866.
HSSP, P41964; IMVN.
GO, GO:0003793; F. defense/immunity protein activity; IEA.
InterPro: IPR00376; Gamma-thionin.
                                                              Picea abies (Norway spruce) (Picea excelsa).
Wararyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 TGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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|YSASpPheHisValAlaAsnArgLysCysTyrCysSerLysProCys
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B94207ADAB8FE4A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                       887
224
24
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        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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Conservative:
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                                            Putative gamma-thionin protein precursor.
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ProDom, PD002594, G Purothionin, 1.
SMART, SM00505, Knotl, 1.
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8835 MW;
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 ProGlyIleCysIleThrLysProProCysArgLysAlaCysIleLys---GluLysPhe
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
NCBI_TaxID=157791;
                            SEQUENCE FROM N.A.

McKendree W.L., Doostdar H., McCollum T.G., Mayer R.T.;

"CDNA cloning and expression of a gene (Accession No. Z97064) from

"Chrus paradisi roots similar to bacterial YRN1 and HEAHIO proteins
and an mRNA from Brassica oleracea that is wound and dark inducible
(PGR97-127).";
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to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                          B7C586CE8DB565DF CRC64;
                                                                                                                                                                        EMBL, AB005266, BAA21114.1; -... CG. GO.003993, F:defense/Ammunity protein activity; InterPro; IPR008176, Gamma-thionin.
InterPro; IPR008176, Gamma-thionin.
Pfam; PF00304; Gamma-thionin, 1.
Prodom; PD002594; G Purothionin; 1.
SWART; SM00505; Kncli; 1.
SWART; SM00505; Kncli; 1.
SEQUENCE 105 AA; 11635 MW; B7C586CE8DB565DF CRC64,
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Submitted (JUN-1997)
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01-OCT-2003
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InterPro; IPR003614; Knot1.
Pfam; PF00304; Gamma-thicnin; 1.
ProDom; PD002594; G_Purothionin; 1.
SMART; SM00505; Knot1; 1.
SEQUENCE 75 AA; 8631 MW; 6ACS70E92D88013E CRC64;
                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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112.00
45.33%
37.33%
14.89%
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Percent Similarity:
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Best Local Similarity:
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Query Match:
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US-10-006-252A-19 (1-414) x Q8W434 (1-75)

Search completed: May 11, 2004, 17:04:29 Job time: 43 secs

May 13, 2004, 08:49:06; Search time 1784 Seconds (without alignments) 10058.305 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-10-006-252A-19 414 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3470272 segs, 21671516995 residues Searched:

6940544 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database :

90 ha: *
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Natch Length DB ID Description			ж			SUMMAKIES		
414 100.0 414 6 A26875 A26874 A39544 A14 100.0 414 6 AR13072 AR13072 AR13071 A14 100.0 414 6 AR13072 A813072 A81	sul No	COL	a te	engt	DB	αi	escription	
414 100.0 414 6 A39549 A3954 414 100.0 414 6 A8750153 A8364 414 100.0 414 6 A8750137 A8730 414 100.0 414 6 A8750131 A8730 414 100.0 414 6 A8750131 A8730 414 100.0 414 6 A8730230 A8730 414 100.0 414 6 A8730230 A8730 54.2 61.4 288 6 A8730200 A8730 54.2 61.4 288 6 A8730200 A8730 54.2 61.4 288 6 A873020 A8730 55.2 61.4 288 6 A873020 A8730 56.0 40.0 8 A8701459 A87014 56.0 40.0 6 A873249 A87014 56.0 6 A873280 A8701450 A8730 56.0 40.0 6 A873280 A8701450 A8730 56.0 40.0 6 A873280 A8701450 A8730 56.0 6 A873280 A8701450 A8730 56.0 40.0 6 A873280 A8701450 A8730 56.0 6 A873280 A8701450 A8701450 56.0 6 A873280 A8701450 A8701450 56.0 40.0 6 A8701450 A8701450 A8701450 56.0 40.0 6 A8701450 A8701450 A8701450 56.0 40.0 6 A8701450 A8701450 A8701450 A8701450 56.0 40.0 6 A8701450	1	414	100.0	· H	9	A26875	6875 R.sat	6
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Dubock, A.C., Fowell, K.A. and Rees, S.B.
ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
Patent: WO 9416076-A 37 21-JUL-1994;
ZENECA LID (GB)
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    414
    /organism="Raphanus sativus"

                             Patent: WO 9305153-A 33 18-MAR-1993;
ICI PLC (GB)
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Location/Qualifiers
                                                                                                                                                                                /mol_type="unassigned DNA"
/db_xref="taxon:3726"
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Sequence 37 from Patent WO9416076.
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A39549.1 GI:2295842
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/db xref="taxon:32644"
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                                                                                             Location/Qualifiers
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Matches 414; Conservative
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Patent: WO 9721814-A 19 19-JUN-1997,
ZENECA LTD (GB)
Other publication AU 1105397 19970703.
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/mol_type="unassigned_DNA"
/db_xref="taxon:32644"
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Sequence 19 from Patent W09721814.
A63404
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ORGANISM REFERENCE AUTHORS

JOURNAL FEATURES

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1 (bases 1 to 414)
Brocksert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Blocklal proteins
Patent: US 6187904-A 48 13-FEB-2001;
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/organism="unknown"
/wol_type="unassigned DNA"
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from patent US 5538525.
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Matches 414, Conservative
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              PAT 16-MAY-2001
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Brockeert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Blocidal proteins
Patent: US 5824869-A 48 20-OCT-1998;
Location/Qualifiers
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100.0%; Score 414; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 414; Conservative 0; Mismatches 0; Indels
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Sequence 48 from patent US 5824869.
AR050153
AR050153.1 GI:5972145
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Sequence 48 from patent US 6187904.
AR130272
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100.0%; Score 414; DB 6; Length 4 100.0%; Pred. No. 5e-88; ive 0; Mismatches 0; Indels
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Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Terras, P.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 5538525-A 48 23-JUL-1996;
Location/Qualifiers
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GITCITITIGCIGCITICGAAGCACCAACAAIGGIGGAAGCACAGAAGTIGIGCGAAAGG 120
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Broekaert, W.Frans. and Rees, S.Bronwen. Antifungal proteins
Patent: US 6372888-A 19 16-APR-2002;
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Matches 414; Conservative
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1 (bases 1 to 414)

1 (bases 1 to 414)

Sijtsma.L., Pant.F., Borremans, F.A., De Samblanx, G.W., Sijtsma.L., Meloen, R.H., Puijk, W.C., Schaaper, W.M., Brockaert, W.R., van Galder, W.M.. and Rees, S.B.
Antifungal peptides and composition thereof
Patent: US 6605698-A 45 12-AUG-2003;
Location/Qualifiers
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Sequence 45 from patent US 6605698.
AR374914
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/organism="unknown"
/mol_type="genomic DNA"
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269 TATTTCCCTTGTTAATTCCATAAACTCTTCGGTGGTTAATAGTGTGCGCATTTTACATAT 328
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/function="antifungal, fungistatic"
/function="antifungal, fungistatic"
/functe="Evidence for antifungal activity: Analysis of two novel classes of antifungal proteins from radish (Raphanus sativus L.) seeds. _Terras, F.R.G. et al. (1992), J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="antifungal protein 1 preprotein"

/protein id="AAA69541.1"

/brotein id="AAA69541.1"

/brotein id="AAA69541.1"

/translation="warkasilalipraalvirpaareapTMVEAQKiCERPSGTWSGVCGNNNACKNQCINLEKARHGSCNYVFPAHKCICYFPC"
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1 (sites)
Perras, FX. G., Eggermont, K., Kovaleva, V., Raikhel, N.V.,
Osborn, R.W., Kester, A., Rees, S.B., Torrekens, S., Van Leuven, F.,
Vanderleyden, J., Cammue, B.P.A. and Broekaert, W.F.
Small cysteine-rich antifungal proteins from radish: their role in
                                                                                                                                                                          Direct Submission
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
G Generics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-3001
On Feb 9, 1995 this sequence version replaced gi:609321.
Location/Qualifiers
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100.0%; Pred. No. 2.8e-83;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  forganism="Raphanus sativus"
mol_type="mRNA"
strain="ronde rode kleine witpunt"
db_xref="taxon:3726"
tissue_type="seed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function="antifungal, fungistatic"
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/note="18 A nucleotides"
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Chem. 267, 15301-15309"
/citation=[1]
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Plant Cell 7, 568-573 (1995)
2 (bases 1 to 395)
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102. .254
/gene="Rs-AFP1"
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gene="Rs-AFP1"
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94; Conservative
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Best Local S
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C12N15/09, A01H5/00, A01N65/00, C07X14/415, C12N1/21, C12N5/10// PC (C12N15/09, C12R1:91), (C12N1/21, C12R1:91), (C12N5/10, C12R1:91), PC
                                                                                                                                                                                                                            E34290 DNA linear PAT 31-JAN-2002 bage and plasmid constructed by ligating antibacterial protein gene DNA with vector DNA, transformant microorganism and transformant plant containing the same and antibacterial protein.
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362
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                      302 AAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTATATGT
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  303 AAAATAAGTCAGTGTCACTATCCATGAGTGATTTTTAAGACATGTACCAGATATGTTATGT
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Pred. No. 3e-50;
                                                                                 396
                                                                                                         362 IGGIICGGITATACAAATAAAGTITIATICACCA 395
                                                                                 363 IGGITCGGITATACAAATAAAGITTTATICACCA
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2000116379-A/1.
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Best Local Similarity 81.0%;
Matches 333; Conservative
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240

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PAT 16-MAY-2001
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Brockaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 6187904-A 58 13-FEB-2001;
Location/Qualifiers
                                                                             Length 288;
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Pred. No. 4.9e-50;
0; Mismatches 3;
                                                                             61.4%; Score 254.2; DB 6;
ilarity 98.8%; Pred. No. 4.9e-50;
Conservative 0; Mismatches 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AR130280 288 bp I Sequence 58 from patent US 6187904. AR130280.1 GI:14118177
1. .288
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/wol_type="unassigned DNA"
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98.8%;
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256; Conservative
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Unclassified.
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     301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATG-TTA 359
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Dubock,A.C., Powell,K.A. and Rees,S.B.
ANTHMCROBIAL-PROTBIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
PATENT: WO 9416076-A 41 21-JUL-1994;
ZENECA LTD (GB)
                                                                    389 TGTTGGTTTGGTTATATATAAAAAGTTTACGGATATAATAAGATGATAA 439
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Other publication AU 5820494 940815
Location/Qualifiers
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Sequence 58 from patent US 5824869.
AR050161. GI:5972153
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Sequence 41 from Patent WO9416076.
A39553
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Direct Submission
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
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Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.

Brical proteins

Patent: US 5538525-A 58 23-JUL-1996;

Location/Qualifiers
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Plant Cell 7, 568-573 (1995)
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sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
Chem. 267, 15301-15309"
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Pred. No. 5.1e-49;
0; Mismatches 76; Indels
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of Genetics, Applied Biological Sciences,
Heverlee, Belgium, B-3001
Location/Qualifiers
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3373863 segs, 2124099041 residues Searched:

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Database :

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178.8	17	156.8	154.2	153.6	153.6	152.4	152.4	151.4	147.6	145.8	145.8	145.4	145	144.6	144.2		144.2		129.8	104.2	
24	25	26	27	28	29	30	31	32	33	34	3	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

AAQ38650 standard; DNA; 414 BP. (revised)
(first entry) RS-AFP1 CDNA. 25-MAR-2003 07-JUL-1993 AAQ38650; AAQ38650

Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.

Raphanus sativus.

Location/Qualifiers 16. .256 /*tag= a 92WO-GB001570. 27-AUG-1992; WO9305153-A1 18-MAR-1993

91GB-00018523. 92GB-00003038. 92GB-00013526. 29-AUG-1991; 13-FEB-1992; 25-JUN-1992;

(ICIL) IMPERIAL CHEM IND PLC.

Terras FRG; Rees SB, Broekaert WF, Cammue BPA, Osborn RW, Vanderleyden J;

WPI; 1993-100978/12.

Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial diseases.

Example 21; Fig 35; 110pp; English.

This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. primer AAQ38640 was used together with AAQ38641 to generate a probe

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screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage then into the pBluescript phagemid form with the aid of helper phage then incompared by agarose gel electrophoresis. Four clones had insert sizes of approx. 400bp the others between 250-300bp. The inserts of the 4 largest clones were then sequenced and found to differ only in the length of their S' and 3' UTK's. The longest sequence is given here.
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Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

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Query Match 100.0%; Score 414; DB 2; Best Local Similarity 100.0%; Pred. No. 3.8e-92; Matches 414; Conservative 0; Mismatches 0;
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AAQ70128 standard; cDNA; 414 25-MAR-2003 14-FEB-1995 AAQ70128; RESULT 2

(first entry) Antimicrobial Rs-AFP1. (revised)

Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.

Raphanus sativus.

21-JUL-1994

WO9416076-A1

94WO-GB000012. 05-JAN-1994;

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GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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                                                                                                                                                                                                                                                                                                                        Plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA sequence of Rs-AFP1 is given in AAQ70128. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
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100.0%; Pred. No. 3.8e-92;
iive 0; Mismatches 0;
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  93GB-00000281.
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                                                                                     Dubock AC, Powell KA,
                                                                                                                                  WPI; 1994-249223/30.
                                        (ZENE ) ZENECA LID.
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08-JAN-1993;
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180 180 300

414

361 361

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Raphanus sativus antifungal protein I (Rs-AFP1) cDNA AAT72333 standard; cDNA; 414 BP (first entry) (revised) 25-MAR-2003 19-JAN-1998 AAT72333; RESULT 3 AAT72333

Antifungal protein; candida; fungal resistance; food additive; radish; crop protection; plant defensin; bacterial protection; preservative; ss.

Raphanus sativus.

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241 TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
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                                        ACAAAATAAGTCAGTGTCATATCCATGAGTGATTTTTAAGACATGTACCAGATATGTTAT
                                                                            301 ACAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT
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                                                                                                                  Rs-AFP1; radish antifungal protein 1; fungicide; salt tolerance;
preservative; transgenic plant; crop protection.
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/transl except= (pos:85. .87, aa:Glu)
16. .102
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100.0%; Pred. No. 3.8e-92;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This cDNA sequence encodes an Rhapanus sativus (radish) antifungal protein (Rs-AFP1). Analogues of the homologous protein, Rs-AFP2 (AAM19281), have also been produced (see AAM19282-92, AAM1928-98, AAM19310-04, AAM19310-34 and AAM31765-8314). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease tolerance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of the first protect plants by introducing them, or a microorganism capable of the first parts of the soil. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as
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Borremans FAM, Rees SB;
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                                                        .87, aa:Glu)
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100.0%; Pred. No. 3.8e-92;
ilve 0; Mismatches 0;
                                                                                                                                /*tag= c
/product= "antifungal_protein_1"
                                                        (pos:85.
                                                                                                                                                                                                                                                                                                                                                                                                  Schaaper WMM,
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutic or preservative agent.
                                    /*tag= a
/transl_except=
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96GB-00006552.
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                                                                      /*tag= L
255
                    .258
                                                                    . 102
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nes 414; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Puijk WC,
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                                                                                                                                                                                                                                                                                                                                                            (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW19280.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Gelder WMJ;
                                                                                                                                                                                                                                                                                                                                                                              Meloen RH, Pu
                                                                                                                                                                                  WO9721815-A2
                                                                                                                                                                                                                                                                12-DEC-1996;
                                                                                                                                                                                                                                                                                                      13-DEC-1995;
                                                                                                                                                                                                                                                                                                                      28-MAR-1996;
                                                                      sig_peptide
                                                                                                                                                                                                                        19-JUN-1997
                                                                                                            mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well
                        GITCITITICCICCITICGAAGCACCACAATGGTGGAAGCACACAGAAGTTGTGCGAAAG
                                                                                                                                                     AACCTIGAGAAAGCACGACAIGGAICTIGCAACTAIGICTICCCAGCTCACAAGTGIAIC
                                                                                                                                                                                                                  241 TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC
 GTTCTTTTTGCTGCTTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
                                                                                              121 ccaachicecaiceichachaichicighaanchairaacecaiceangaaicheigearr
                                                                                                                               AACCITGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
                                                                                                                                                                                                                                                            ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT
                                                              CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
                                                                                                                                                                                                                                                                                                                            /product= "Brassica oleracea defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       composite disease resistance; pathogenic bacteria; rice white laaf blight; brown-stribe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica oleracea defensin protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antimicrobial protein; defensin; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; SEQ ID NO 1; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-SEP-2001; 2001JP-00283117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC51221 standard; DNA; 394
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P-PSDB; ADC51222.
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                                                                                                                                                                                                                                                                                                                                   75
                                                                                                                                                                                                                                                                                                                                                                                               9
as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
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                                                                                                                                                                                                                                                                                                                            16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            composite disease resistance; pathogenic bacteria; rice white leaf blight, brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                                                                                                   78.2%; Score 323.8; DB 9; Length 394;
                                                                                                                                                                                                                               .6e-70;
es 37; Indels
                                                                                                                               Seguence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antimicrobial protein; defensin; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
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                                                                                                                                                                                                                               Local Similarity 90.4%; Pred. No. 5.6e es 357; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica defensin protein coding sequence.
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Matches
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AATTAATAAGTITGIGICACTATITATTAGTGACTITTATGACATGTGCCAGGTATGTTTA 388
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                                                                                                                                                                                                                                                                                                                    Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance rice paddy against pathogenic microbes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AGTGGGACATGAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GITITITICIGCTITICGAAGCACCAACAACAATGGTGGAAGCACAGAAGTTGTGTGTCAGAAGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
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Pred. No. 4.7e-53;
0; Mismatches 74; Indels
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16. .256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 4; 7pp; Japanese.
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(first entry)
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                                                                                                                      (TOYA-) TOYAMA KEN
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P-PSDB; AAY91117
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                                      09-OCT-1998;
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07-JUL-1993
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                                                           Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195
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                                                                                                                                                                                                                                                                                               The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 ATGCCTAAGTTTGCGTCCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTTGCTGCT
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pathogenic microbe; radish; rice blast disease; ds.
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                                                                                                                                                                                                                   Claim 3; SEQ ID NO 3; 34pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                     This cDNA represents the sequence of Rs-APP2 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to camino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 1239p product, which was further reamplified with the same primers and digoxigenin-11-durp instead of drTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII CDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage vivo into the pBluescript phagemid form with the aid of helper phage vivo into the pBluescript phagemid form with the aid of helper phage their size compared by agarces gel electrophoresis. Four clones had inserts of approx. 400bp the others between 250-300bp. The inserts of approx. 400bp the others between 250-300bp. The inserts as Rs-AFPI (AAQ38650). Rs-AFP2 was seen to differ by only 2 amino acids from Rs-AFPI, so the Rs-AFPI cDNA was transformed to the Rs-AFP2 nucleotide sequence by PCR assisted site directed mutagenesis. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GITCITITITGCTGCTTTCGAAGCACCAAAAAGGTGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GITCITITIGCIGCITICGAAGCACCAACAATGGIGGAAGCACAGAAGTIGIGCCAAAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AGACTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATAC 240
                                                                                                                                                                                                                                                                                   Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GITTTAITAGIGATCAIGGCTAAGITIGCGICCAICAICGCACTICITITIGCIGCICTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.4%; Score 254.2; DB 2; Length 261; 98.8%; Pred. No. 6.5e-53; ive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                            Terras FRG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                            Rees SB,
                                                                                                                                                                                                            Cammue BPA, Osborn RW,
                                                                                                                                                                                                                                                                                                                                               Example 21; Fig 35; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 recraciriocrideridai 259
                                                                                                                                                                              (ICIL ) IMPERIAL CHEM IND PLC.
                                                                                                                    91GB-00018523.
                                                                                                                                    92GB-00003038.
                                                                                        92WO-GB001570.
                                                                                                                                                  92GB-00013526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCTACTTTCCTTGTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 98.8
Matches 256; Conservative
 /*tag=
                                                                                                                                                                                                                                                        WPI; 1993-100978/12.
                                                                                                                                                                                                                            Vanderleyden J;
                                                                                                                                                                                                           Broekaert WF,
                                                                                        27-AUG-1992;
                                                                                                                    29-AUG-1991;
                                                                                                                                    .3-FEB-1992;
                                                                                                                                                 25-JUN-1992;
                             WO9305153-A1
                                                          18-MAR-1993,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                                                                                     Antimicrobial, Rs-AFP2; symbiosis; disease-resistance; fungus-resistance, Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFP1 from R. sativus. The full-length CDNA sequence of PCR assisted atte-directed mutagenesis of Rs-AFP2 is given in AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCCAAAGG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAGTGTATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AGACTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTAIC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 GIITITAITAGIGAICAIGGCIAAGIIIGCGICCAICAICAICGACIICIITIIGCIGCICII 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GITIIAFIAGIGATCAIGGCIAAGIFIIGCGICCAICAICGCACIFCTTTIIGCIGCICIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GTTCTTTTGCTGCTTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 ccaagrodgacargercaggacricrogaaacaaraacgcargcaagaarcagrocarr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.4%; Score 254.2; DB 2; Length 288; 98.8%; Pred. No. 6.6e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                     PCR; polymerase chain reaction; mutagenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 33; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TGCTACTTTCCTTGTTAAT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 TGCTACTTTCCTTGTTAAT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rees SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-GB000012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93GB-00000281.
                        AAQ70130 standard; cDNA; 288
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 256; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dubock AC, Powell KA,
                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                        Antimicrobial Rs-AFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-249223/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raphanus sativus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR57327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9416076-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JAN-1993;
                                                                                                                                                        25-MAR-2003
14-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1994.
                                                                                        AAQ70130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
AAQ70130
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191 AACCTTGAGAAAGCACGACATGGAACTATGTCTTCCCAGCTCACAAATGTATC 250
                                                            241 TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
                                                                                                                                                                               311 CTATTAAATAAGTATGTGTCACTCTATGAGAGGTCTTATGACATGTACCAGATATGTTAT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein and the antifungal protein 2 (RsAFD2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is posttranslationally processed into the component protein molecules. The propeptide sequence is rich in amino acide A, V, S and T and contains diperbidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
protein expression; plant defensin; RSAFP2; antifungal protein; AFP2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
                                                                                                  251 ricciacitroccarditraarcraccaagaccrcritaargcritaararraaagrgrafitr
                                                                                                                                          301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTTAAGACATGTACCAGATATGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
3. .566
/product = "fusion protein of DmAMP1 and RsAFP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding a fusion protein of DmAMP1 and RSAFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Bolle MFC,
                                                                                                                                                                                                                                                           371 Grigcrirarrahaggrahactir 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 34; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Francois IEJA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-GB002716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98GB-00018001
98GB-00026753
                                                                                                                                                                                                                                                                                                                                                           AAZ99339 standard; DNA; 575
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-246564/21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY84072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dahlia merckii.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200011175-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .8-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                   AAZ99339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GITITICITITICITICITICITICAAGCACCGATGGTGGAAGCACAGAAGTTGTGCGAGAGG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GITCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 CCAAGTGGGACATGGTCCGGAGTTTGCGGAAACAGTAACGCGTGCAAGAATCAGTGCATT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGGTCACAAGTGTATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes the Arabidopsis PDF1.1 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensing gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Manners JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GITTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                  PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Terras FRG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7e-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penninckx IAMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 242.4;
Pred. No. 5.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "plant defensin"
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           "PDF1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 72pp; English.
                                       AAV10632 standard; DNA; 403 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.6%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-GB001672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96GB-00013753,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomma BPHJ,
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                     /*tag=
/*tag=
.113
                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
114. .265
                                                                                                                                                                                                                                                                                                                                                                              Д
                                                                                                                                                                                                                                                                                                                                                                                                                                         product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 297; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                                                                                                          A. thaliana PDF1.1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene from Arabidopsis.
                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-086663/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZENE ) ZENECA LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW40345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Broekaert WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9800023-A2
                                                                                                                   23-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JAN-1998
                                                                                                                                                                                                  Defensin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                             AAV10632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
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This sequence encodes the Arabidopsis PDF1.2 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                    Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;
Disclosure, Fig 1; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-503109/46.
                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-1997.
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                                                                                                                                                                                                                                                                                                            245
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                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
                                                                                     377
                                                                                                          GCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGG 129
                                                                                                                             ecrecriricgaagcaccaacaargergaagcacagaagrigigcaaagccaaagrcgr 437
                                                                                                                                                  ACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAG 189
                                                                                                                                                                  acaregreaegacrereregaaacaaraacearecaagaareagacreaegacreaega 497
                                                                                                                                                                                        AAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTT 249
                                                                                                                                                                                                   6,9
                                                                                      GGGCCCATGGCTAGGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCTTTTT
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                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
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                             Length 575
          Seguence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 U; 0 Other;
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                                                                     GIGAICAIGGCIAAGIIIIGCGICCAICAICGCACIICIIIIIIGCIGCI
                                                Indels
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                             DB 3;
                           / Match 56.1%; Score 232.4; DB 3 Local Similarity 95.6%; Pred. No. 1.8e-47; Nes 239; Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penninckx IAMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.319
/*tag= b
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/product= "PDF1.2"
/note= "plant defensin"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
32. .274
                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9800023-A2
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                                                                                                                                                                                                                                                                                                                                                              A. thaliana
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                             Query Match
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                                         Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTITICCTIGITAATITTATIGGAAACTICTTIGGIGAATAGTITTTTATGTAATITTACAAA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accrecenterralarenecernarientregreenaareerenentriaenaaa 320
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                                                                                                                                                                                                                                                                                           5 TATTAGEGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTTGTTC
                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi.
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53.9%; Score 223; DB 2; Length 400; 79.9%; Pred. No. 3.3e-45; Indels ive 0; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATAAGTCAGTGACTATCCATGAGTGATTTTAAGACATGTA
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                                                                                                                                                         Matches 274; Conservative
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(IWAT-) IWATE KEN.
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               30-APR-1998;
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01-MAR-2000
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           This sequence represents the cDNA sequence encoding the antifungal polypeptide AlyAFP, from plants of the genus AlySeum. The sequence represents a composite of the sequences isolated by 5' and 3' RACE (Rapid Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The AMPAPP to 'ColyPeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                             59 AGTAATAGATATGGGCTAAGTGTGCGTTCCATCTCCCTTGTCTCTGCTGCTGTTCT 118
                                                                                                                                                                                                                                                                                                          126 TGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCT 185
                                                                                                                                                                                                                                                                                                                                                              186 TGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTA 245
                                                                                                                                                                                                                                                      TTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAG 125
                                                                                                                                                                                                                                                                             119 CTTTGCTGCTTTTGAAGCACCAGCAATGGTGGAGTCACGGAAGTTGTGCGAAGATCCAAG 178
                                                                                                                                                                                                                                                                                                                                                                                        239 reanheadchachachartrachachartrachachachachachanganhartracha 298
                                                                                                                                                                                                                                                                                                                                                                                                                                             299 chicccandinabichaccaarcacriningiecrigrengrenarinacardinaie 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTTTATTTACATGAATAAGTCTGTGTCA-TCCTTATGGGTGACCTTATGACATGTACC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 AGATATGTTAT-----GTTGGTTCGGTTATACAAATAAAGTTTTATTCACCAA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418 AGATATATCATATATGTATGTTGGTTTGTGTGGCCAATTATAAACTTTTATTGTGGA 477
                                                                                                                                                                                                                                                                                                                                     redaacardecargrerereresaaraaraacecarecaagaacearecaarecaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wasabia japonica antibacterial protein encoding cDNA SEQ ID NO:1.
                                                                                                                                             Query Match 49.1%; Score 203.4; DB 2; Length 500; Best Local Similarity 72.5%; Pred. No. 2.3e-40; Matches 317; Conservative 0; Mismatches 91; Indels 29,
                                                                                                                                                                                                 6 ATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCT
                                                                                                                   Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;

    243
    *tag= a
    /product= "antibacterial protein"

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                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTCCTTGTTAATTTATCGCAAACTCTTTGGTG-
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01-MAR-2000
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                                                                                                                                                                                                                                                                                                                                     179
                                                                                                                                             Query Match
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The present sequence encodes an antibacterial protein isolated from Wasabia japonica. The antibacterial protein can be used as a food or feed additive. (Updated on 15-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TCAGGAGTCTGTGGAAACAATGCGTGCAAGAATCAGTGCATCAACUTTGAGGGAGCA 180
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                                                                                                                                                                                                                        An antibacterial protein gene of Wasabia japonica - useful as a food- or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TTTGAAGCACCATCAATGGTGGAAGCGCAGAAGTTGTGGTGGAAAGTCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
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Pred. No. 3.5e-40;
0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wasabia japonica; antibacterial; food additive; ds.
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/product= "antibacterial protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ39124 standard; cDNA to mRNA; 416 BP.
                                                                                                                                                                                                                                                                                                                    Claim 3; Page 12-13; 16pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
98JP-00121303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.98;
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.43
Matches 220; Conservative
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                                                                                                                         WPI; 2000-057353/05
                                                         (IWAT-) IWATE KEN.
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XX
DR P-PSDB; AAY57565.
XX
An antibacterial protein gene of Wasabia japonica - useful as a food- or PT feed-additive.
XX
Claim 3; Page 13-14; 16pp; Japanese.
XX
CC The present sequence encodes an antibacterial protein isolated from CC Wasabia japonica. The antibacterial protein can be used as a food or feed CC additive. (Updated on 15-SEP-2003 to standardise OS field)
XX
Sequence 416 BP; 111 A; 77 C; 81 G; 147 T; 0 U; 0 Other;
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0 ;	75	60	135	120	195	180	255	240		
Ouery Match Best Local Similarity 88.0%; Pred. No. 8.6e-40; Matches 219; Conservative 0; Mismatches 30; Indels 0; Gaps	16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT	1 AIGGCTAAGITTGCTTCTATCATCGCTCTTCTTCTTCTTCTTCTTCTTTTTTTT	76 TICGAAGCACCAACAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGGAGACATGG	TTTGAAGCACCATCAATGGTGGAAG	136 TCAGGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195	1 TCAGGAGTCTGTGTATACAAACAATGCGTGCAAGCATCAGTGCATCAACCTTGAGGAGCA	S CGACATGGARCTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT	CGACATGGATCTTGCAACTATCTTCCCATATCACAGATGTATCTGTTACTTCCCATGT	256 TAATITAIC 264	241 TAATTATTC 249
Matc] ocal s 2:	ř	••	7,	61	136	121	196	181	256	24
Query Match Best Local Matches 21	ò	đ	δ	원	ò	qq	ογ	Q	ò	d d

Search completed: May 13, 2004, 09:41:02 Job time : 355 secs

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; LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48,
Sequence 19,
Sequence 45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 48,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1
Sequence 1
Sequence 9
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*

(cgn2_6/ptodata/2/ina/6B_COMB.seq:*

(cgn2_6/ptodata/2/ina/6A_COMB.seq:*

(cgn2_6/ptodata/2/ina/B_COMB.seq:*

(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-777-192-48

US-09-077-951-19

US-09-077-951-19

US-09-077-988-45

US-08-377-688-45

US-08-377-688-58

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US-09-103-489-14

US-09-103-489-14

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US-09-103-489-14

US-09-103-489-14
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                                                                                                                                                                                                                                                                                                                          682709 seqs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                      - nucleic search, using sw model
                                                                                                                                                                                                                                                                     IDENTITY NUC Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Match Length
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                                                                                                                                                                                                               Perfect score:
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Maximum DB seq
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US-08-777-192-50

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US-08-377-687-34

US-08-377-687-34

US-08-777-192-34

US-08-971-982-34

US-08-971-982-34

US-08-971-982-34

US-08-777-192-31

``

ALIGNMENTS

APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. Sequence 48, Application US/08377687 Patent No. 5538525 GENERAL INFORMATION: STREET: 1100 NCITY: WASHINGT STATE: D.C. COUNTRY: USA ZIP: 20005

COMPUTER EADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
FILING DATE: CLASSIFICATION BATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-7AN-1993
ATTCRNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 19942/SEE.36525/US/A
TELEPRONES, 202-861-3000
TELEFAX: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
TYPE: nucleic acid

linear TOPOLOGY: lir MOLECULE TYPE:

CDS 16..255

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INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS
 NAME/KEY:
LOCATION:
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 US-08-777-192-48
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 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
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 Length 414;
 0; Indels
 100.0%; Score 414; DB 1; L
100.0%; Pred. No. 7.4e-107;
ive 0; Mismatches 0;
 OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
 99042/SEE.36525/US/A
 APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUND P.A.
APPLICANT: CAMMUE, BRUND P.A.
APPLICANT: TERES, SARAH B.
APPLICANT: TERESAS, FRANKY R.G.
APPLICANT: TERESAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 CLASSIPICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-DAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 99042/SEE.3
REFERENCE/DOCKET NUMBER: 99042/SEE.3
TELEPHONE: 202-861-3000
 STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
 ; Sequence 48, Application US/08777192; Patent No. 5824869

 Floppy disk
 IBM PC compatible

 Query Match
Best Local Similarity 100.
Matches 414; Conservative
 202-822-0944
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 COMPUTER: IBM PC OPERATING SYSTEM:
 GENERAL INFORMATION:
 FILING DATE:
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 US-08-777-192-48
 COUNTRY:
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 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 240
 241 IGCTACTTTCCTTGTTAATTTATCGCAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
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 61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAAAAGTTGTGCGAAAGG
 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT
 0;
 Length 414;
 Indels
 1 GITITATIAGIGATCAIGGCIAAGITIGCGICCAICAICGCACTICI
 MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 17-NO. 6187904-1997
 100.0%; Score 414; DB 1; L
100.0%; Pred. No. 7.4e-107;
ive 0; Mismatches 0;
 ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA ZIP: 20005
COMPUTER READABLE FORM:
 REES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BICCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
 Sequence 48, Application US/08971982
Sequence 48, Application US/08971982
Patent No. 6187904
GENERAL INFORMATION:
APPLICANT: BROBKAERT, WILLEM F.
CAMMUE, BRUNO P.A.
OSBORN, RUPERT W.
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNES: both
TOPOLICY: linear
MOLECULE TYPE: CDNA
 Query Match
Best Local Similarity 100."
Matches 414; Conservative
 CDS
16..255
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9

180 240 240 300

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61 GITCITITICCITICGAAGCACCAACAAGGIGGAAGCACAGAAGTIGTGGGAAAGG 120
 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
 241 IGCTACITICCTIGITAATTIATCGCAACTCTTIGGTGAATAGTTTTTATGTAATTTAC 300
 61 GTICTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
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 GITTIATIAGIGATCATGGCTAAGITTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
 241 IGCTACTITCCTIGITAATTTAICGCAAACTCTTIGGIGAATAGTTTTAIGTAATTTAC
 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT
 Gaps
 ;
0
 Length 414;
 1 GITTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTT
 0; Indels
 100.0%; Score 414; DB 4; L 100.0%; Pred. No. 7.4e-107;
 APPLICANT: DOLIEMENTS, FIGURE
APPLICANT: Sitjtsma, Lolke
APPLICANT: Sitjtsma, Lolke
APPLICANT: Sitjtsma, Lolke
APPLICANT: Puijk, Wouter
APPLICANT: Puijk, Wouter
APPLICANT: Poijk, Wouter
APPLICANT: Prockart, Wilhelmus
APPLICANT: Breckart, Willem
APPLICANT: Wan Gelder, Wilhelmus
APPLICANT: Nan Gelder, Wilhelmus
APPLICANT: 1994-6-257(SyN-035)
CURRENT FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-13
NUMBER: OF SEQ ID NOS: 141
SOUTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: ANA
 0; Mismatches
 Sequence 45, Application US/09077948A Patent No. 6605698
 Van Amerongen, Aart
Fant, Franky
Borremans, Frans
 ; NUMBER OF SEQ ID NOS: 77
; SOFWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Raphanus sativus
US-09-077-951-19
 Query Match
Best Local Similarity 100.(
Matches 414; Conservative
 TYPE: DNA ORGANISM: Raphanus sativus
 GENERAL INFORMATION:
 US-09-077-948A-45
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 61 GTTCTTTTTGCTGCTTTCGAAGCACCACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 240
 241 IGCTACTTICCTIGITAATITTAICGCAAACTCTTIGGIGAATAGTITTTAIGTAATITTAC 300
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 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCCAGCTCACGAGTGTATC
 1 GITITATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTT
 1 Grinariagranicardecraagringcerccarcardecacriningcrecrer
 Gaps
 ;
0
 Query Match 100.0%; Score 414; DB 3; Length 414; Best Local Similarity 100.0%; Pred. No. 7.4e-107; Matches 414; Conservative 0; Mismatches 0; Indels
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/002,480

FILING DATE: 04-0AN-1993

ATTORNEY AGENT INFORMATION:

NAME: KCKULIS, PAUL N:

REGISTRENCE DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:

TELEFRO: 202-661-3000

TELEFRX: 202-6944

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:
 GENERAL INCRMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: De Samblanx, Genoveva
APPLICANT: Brockaert, Willem
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: PPD50093
CURRENT APPLICATION NUMBER: US/09/07,951
CURRENT FILING DATE: 1999-03-11
BEARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1996-12-13
 , NAME/KEY: CDS
; LOCATION: 16..255
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-971-982-48
CLASSIFICATION: <Unknown>
 Sequence 19, Application US/09077951
Patent No. 6372888
 LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
 TOPOLOGY: linear MOLECULE TYPE: cDNA
 FEATURE
 -09-077-951-19
 121
 61
 361
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Query Match
Best Local S
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 61 GITCITITIGCIGCITICGAAGCACCAACAATGGIGGAAGCACAGAAGITGIGCGAAAGG 120
 61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAAGGCATGCAAGAATCAGTGCATT 180
 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAGTGTATC 240
 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
 241 IGCTACTITCCTIGITAATITTAICGCAAACTCTTIGGIGAATAGITTTAIGTAATITTAC 300
 241 recracificerrefratriratescaacicificereaaraciritates 300
 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
 9
 1 GITITATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
 0; Gaps
 414
 100.0%; Score 414; DB 4; Length 414; 100.0%; Pred. No. 7.4e-107; ive 0; Mismatches 0; Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
 REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
 GENERAL INFORMATION:
PATENT ON STATEMENT OF
 ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
 FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY AGENT INFORMATION:
 ; Sequence 58, Application US/08377687
; Patent No. 5538525
 Matches 414; Conservative
 ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
 Query Match
Best Local Similarity
 USA
US-09-077-948A-45
 RESULT 6
US-08-377-687-58
 COUNTRY:
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61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
 208 AGACTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATTC 267
 88 GIICITITIGCIGCITICGAAGCACCAACAAIGGIGGAAGCACAGAAGITIGIGCCAAAAGG 147
 148 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 207
 9
 28 GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCGCACTTCTTTTTGCTGCTCTT 87
 1 GITTITATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
 0; Gaps
 61.4%; Score 254.2; DB 1; Length 288; 98.8%; Pred. No. 3.9e-62; ive 0; Mismatches 3; Indels 0
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: TERES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
ITILE OF INVENTION: BLOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
 ADDRESSE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-03N-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
 APPLICATION NUMBER: US/08/777,192 FILING DATE:
 Sequence 58, Application US/08777192
Patent No. 5824869
GENERAL INFORMATION:
 241 TGCTACTTTCCTTGTTAAT 259
 268 IGCIACTITICCTIGITAAT 286
 APPLICANT: BROEKAERT, WILLEM F. APPLICANT: CAMMUE, BRUNO P.A. APPLICANT: OSBORN, RUPERT W.
 58:
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic.acid
STRANDEDNESS: both
 Matches 256; Conservative
 NAME: KOKULIS, PAUL N. REGISTRATION NUMBER: 1
 TOPOLOGY: linear
MOLECULE TYPE: cDNA
PEATURE:
 43..282
 Similarity
 CLASSIFICATION:
 NAME/KEY: CDS
 20002
 STATE: D.C
 ,
US-08-377-687-58
 US-08-777-192-58
 COUNTRY:
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121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 61 GITCTITITGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
 208 AGACTIGAGAAAGCACGACAIGGAICTIGCAACTAIGICTITCCCAGCICACAGAGTGIAIC 267
 88 dincinitraciacrinicaaagcaccaacaanagaagcacaaagaagingigecaaagg
 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
 28 GirinaliagicalcandeciaaGringceiccarcarcecacriciringcedecien
 1 GITITATIAGIGALCAIGCIAAGITIGCGICCAICAICGCACITCITITIGCIGCICIT
 148 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
 Gaps
 Sequence 16, Application US/08627706

Patent No. 5773596

GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Younie S.
APPLICANT: Wo. Younie S.
APPLICANT: Wo. Younie S.
APPLICANT: Rosenberger, Clindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CONTAINS: MISSOURI
 .
0
 Length 288;
 NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
RELECOMMULCATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-802-0944
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: both
 Indels
 DB 3;
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
 61.4%; Score 254.2; DB 3, 98.8%; Pred. No. 3.9e-62; ive 0; Mismatches 3,
 LOCATION: 43..282
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-08-971-982-58
 241 IGCIACTITCCTIGITAAT 259
 ATTORNEY/AGENT INFORMATION:
 268 IGCIACTITCCTIGITAAT
 TOPOLOGY: linear MOLECULE TYPE: CDNA
 Query Match
Best Local Similarity 98.8
Matches 256; Conservative
 CDS
 ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 NAME/KEY:
 FEATURE
 RESULT 9
US-08-627-706-16
 STATE: M.
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 61 GITCITITIGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATT 180
 88 GITCITITIGCTGCTTTCGAAGCACCAACAATGGTGGAAGGACAGAAGATGTGCCCAAAGG 147
 207
 181 AACCITGAGAAAGCACGACAIGGAICTIGCAACTAIGICTICCCAGGICAAGIGIAIC 240
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 267
 1 GITITATIAGIGATCAIGGCIAAGITIGCGICCAICAICGCACTICITITIGCIGCICIT 60
 148 CCAAGTGGGACATGGTCAGGAGTCTGTGGGAAACAATAACGCATGCAAGAATCAGTGCATT
 208 AGACTIGAGAAAGCACGACAIGGAICIIGCAACIAIGICIICCCAGCICACAAGIGIAIC
 Gaps
 ò
 Length 288;
 Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLING DATE: 17-No. 6187904-1997
CLASSIFFICATION: <understand
 61.4%; Score 254.2; DB 1;
98.8%; Pred. No. 3.9e-62;
 99042/SEE.36525/US/A
 0; Mismatches
 ADDRESSEE: CUSEMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
 APPLICATION NUMBER: US 08/002,480 FILING DATE: 04-JAN-1993
 REES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLEXDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
 Sequence 58, Application US/08971982
Patent No. 6187904
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
CAMMUE, BRUNO P.A.
OSBORN, RUFERT W.
REFERENCE/DOCKET NUMBER: 9904
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-801-3000
TELEPKX: 202-802-0944
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic acid
STRANDENESS: both
 241 TGCTACTTTCCTTGTTAAT 259
 268 idciaciticciiditai 286
 COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
 APPLICATION DATA:
 Query Match
Best Local Similarity 98.88
Matches 256; Conservative
 MOLECULE TYPE: CDNA FEATURE:
 43..282
 linear
 STATE: D.C
 ; NAME/KEY: CDS
; LOCATION: 43...
US-08-777-192-58
 TOPOLOGY:
 US-08-971-982-58
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 61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
 76 GITCICITIGCTGCTTTCGAGGCACCAATGGTGGAGGCACAAAAGTTGTGGGAGGG 135
 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 136 CCATCAGGGACTIGGICAGGAGTCTGCGGAACAACAACGATGCAAGGAACAAGGATC 195
 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
 196 AACCTCGAGAAGGCACGGCATGGATCTTGCAACTACGTCTTCCCAGCTCACAAGAGGGTGCATC 255
 1 GITITAITAGGGATCAIGGCIAAGITIGCGICCAICAICGCACTICITITIGCIGCICTI 60
 16 GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTCCTCTTTGCTGCTCT 75
 Gaps
 Sequence 16, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shah, Dilip M.
APPLICANT: Way, Yonnie S.
APPLICANT: Reachberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
 52.9%; Score 219; DB 1; Length 285; 90.3%; Pred. No. 2.8e-52; Indels tive 0; Mismatches 25; Indels
 E: Charles E. Cohen, Monsanto Company, BB4F 700 Chesterfield Village Parkway No. 6215048th
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMEER: US/09/103,489
FILING DATE: 24-UUN-1998
CLASSIFICATION: 800
 38-21 (10700)A
 ; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

: DESCRIPTION: /desc = "synthetic DNA"

US-08-627-706-16
 NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REGISTRATION NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-624
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 241 TGCTACTTTCCTTGTTAAT 259
 256 TGCTACTTTCCATGCTAAT 274
 ATTORNEY AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
ATTORNEY/AGENT INFORMATION:
 Best Local Similarity 90.3
Matches 234; Conservative
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
 CITY: St. Louis
STATE: Missouri
 63198
 ADDRESSEE:
 RESULT 10
US-09-103-489-16
 COUNTRY:
 STREET:
 Query Match
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Jetus Application US/09829381D

Fatent No. 663200

Fatent No. 663200

GENERAL INFORMATION

APPLICANT: Liang, Jihong

APPLICANT: Rosenberger. Clindy A.

APPLICANT: Rosenberger. Clindy A.

TITLE OF INVENTION: Plant Pathogenic Fungi

TITLE REFERENCE: 38-21 (10700) C.

FILE REFERENCE: 38-21 (10700) C.

FURRENT APPLICATION NUMBER: US/09/829,381D

FILE REFERENCE: 38-21 (10700) C.

FURRENT APPLICATION NUMBER: 09/103,489

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1

SEC ID NO 16

MANGETT LEASE

FURRENT FILE REFERENCE: 28-24

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1

FURRENT FILE REFERENCE: 28-24

MANGETH: 28-5

FURRENT FILE REFERENCE: 28-24

NUMBER OF SEQ ID NO 16

SOFTWARE: PATENTIAL SES
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 61 GTTCTTTTTGCTGCTTTCGAAGCACCACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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 196 AACCTCGAGAAGGCACGGCATGGATCTTGCAACTACGTCTTCCCAGCTCACAAGTGCATC 255
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 0; Gaps
 0; Gaps
 52.9%; Score 219; DB 3; Length 285; 90.3%; Pred. No. 2.8e-52; ive 0; Mismatches 25; Indels
 Query Match 52.9%; Score 219; DB 4; Length 285; Best Local Similarity 90.3%; Pred. No. 2.8e-52; Aatches 234; Conservative 0; Mismatches 25; Indels
REFERENCE/DOCKET NUMBER: 38-21 (10700) A TELECOMMUNICATION INFORMATION: TELEPHONE: (314) 537-6224
 STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
 256 recracrirecarecraar 274
 241 IGCIACTITCCTIGITAAT 259
 TELEFAX: (314) 537-6647
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 TYPE: DNA ORGANISM: Artificial Sequence
 / OTHER INFORMATION: Synthetic US-09-829-381D-16
 Best Local Similarity 90.33
Matches 234; Conservative
 RESULT 11
US-09-829-381D-16
 US-09-103-489-16
 Query Match
 FEATURE:
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121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"

US-09-103-489-17
 ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 ; Sequence 17, Application US/09103489; Patent No. 6215048; GENERAL INFORMATION:
 241 TGCTACTTTCCTTGTTAAT 259
 256 İGCIACTITCCAIGCIAAT 274
 LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 US-09-103-489-17
 COUNTRY:
 92
 121
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 В
 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
 dricicitidecidenticeaedeaectategregaegecacaagingregeseges
 ccarcaddacriddrcaddacridcidaaacaacaacardcaadaacaardcarc
 61 GTICTITITGCIGCITICGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
 76 GITCICITIGCIGCITICGAGGCACCAACTAIGGIGGAGGCACAAAAAGTIGIGCCAAAGG 135
 16 GITITATTAGTGATCATGGCTAAGTTTGCGTCCATCATCATCGCTCTTTGCTGCTCTT 75
 52.1%; Score 215.8; DB 1; Length 285; 89.6%; Pred. No. 2.2e-51; live 0; Mismatches 27; Indels 0
 Sequence 17, Application US/08627706
Patent No. 5773696
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rounie S.
ADDRESSED: Charles E. Cohen, Monsanto Company, BB4F
 ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F STREET: 700 Chesterfield Village Parkway No. 5773696th CITY: St. Louis STATE: Missouri
 1 GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTT
 MEDIUM. --
COMPUTER: IBM PC COMPALILL
CORPUTER: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE: US/08/627,706
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REFISHATION NUMBER: 34,565
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FEBRENCE DOCKET NUMBER: 34,565
FEBRENCE DOCKET NU
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DESCRIPTION: /desc = "synthetic DNA"
 COUNTRY:
ZIP: 63198
COMPUTER READABLE FORM:
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THTTER: IBM PC compatible
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 241 TGCTACTTTCCTTGTTAAT 259
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TYPE: nucleic acid
 Query Match
Best Local Similarity 89.6
Matches 232; Conservative
 single
 linear
 STRANDEDNESS:
 US-08-627-706-17
 US-08-627-706-17
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196 AGACTCGAGAAGGCACGGCATGGATCTTGCAACTACGTCTTCCCAGCTCACAAGTGCATC 255 120 GTTCTCTTTGCTGCCTTTCGAGGCACCAACTATGGTGGAGGCACAAAAGTTGTGCCAAAGG 135 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180 9 75 181 AACCTIGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC GITITATIAGIGATCATGGCTAAGTTTGCGTCCATCATCGCACTCCTCTTTGCTGCTCTC 61 GITCITITIGCIGCITICGAAGCACCAACAATGGIGGAAGCACAGAAGITGTGCGAAAGG Gaps APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: W. Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 70 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri ·. Query Match 52.1%; Score 215.8; DB 3; Length 285; Best Local Similarity 89.6%; Pred. No. 2.2e-51; Matches 232; Conservative 0; Mismatches 27; Indels 0 1 GITITATIAGIGAICAIGGCIAAGITIGCGICCAICAICGCACTICI CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-2107.1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: COLEM. CHAILES E.
REGISTRATION NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 38-21 (10700) A
TELEPHONE: (314) 537-624
TELEPHONE: (314) 537-6047
INFORMATION FOR SEQ ID NO: 17:
SEQUIBNE CHARACTERISTICS:

us-10-006-252a-19.rni

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Matches 317; Conservative 0; Mismatches 91; Indels 29; Gaps
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
 COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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 Search completed: May 13, 2004, 10:54:47
 ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
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 (314) 537-6224
 TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
 TOPOLOGY: linear MOLECULE TYPE: CDNA
 CITY: St. Louis
STATE: Missouri
COUNTRY: USA
 FILING DATE:
CLASSIFICATION:
 63198
 Job time : 85 secs
 TELEPHONE:
 US-08-627-706-9
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 GEREKAL INFOGRATION:
APPLICANT: Shah, Dilip M,
APPLICANT: Shah, Dilip M,
APPLICANT: Shah, Dilip M,
APPLICANT: Wu, Younde S.
APPLICANT: Wu, Younde S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT FILING DATE: 2001-04-09
PRIOR PILING DATE: 1998-06-24
NUMBER OF REQ ID NOS: 20
SOFTWARE: Patentin version 3.1
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 Query Match 52.1%; Score 215.8; DB 4; Length 285; Best Local Similarity 89.6%; Pred. No. 2.2e-51; Matches 232; Conservative 0; Mismatches 27; Indels 0.
 Sequence 9, Application US/08627706
Patent No. 5773696
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Wosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
 ; Sequence 17, Application US/09829381D Patent No. 6653280 ; GENERAL INFORMATION:
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US-08-627-706-9
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 May 13, 2004, 09:35:52 ; Search time 336 Seconds
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 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
 IDENTITY NUC Gapox 1.0
 US-10-006-252A-19
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 Perfect score:
 Scoring table:
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 Sequence:
 Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | Segment 48 Appen | Segmence 45 and   | Semience 19 Appl  | Segmence 58 Appl | Segment 13. Appl | Semience 15 April | Segmenter Con Appendix | Semi-property Semi- | Segmente 16 Appl | Semience 17 Appl  | Frag. 17 aprioring S | Segmence 9 Appli- | Segmence 9 Appli | Sequence 2046, Ap   |
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| SUMMARIES                     | US-09-759-584-48 | US-10-388-361A-45 | US-10-006-252A-19 | US-09-759-584-58 | US-09-732-561-13 | US-09-732-561-15  | US-09-887-576-607      | US-09-829-381A-16   | US-10-681-972-16 | US-09-829-381A-17 | US-10-681-972-17     | US-09-829-381A-9  | US-10-681-972-9  | US-09-938-842A-2046 |
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| %<br>Query<br>Match Length DB |                  | 100.0             |                   | 61.4             | 58.6             |                   |                        |                     |                  |                   |                      | 49.1              |                  | 47.5                |
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| Result<br>No.                 | н                | 7                 | m                 | 4,               | ഹ                | ø                 | 7                      | 80                  | σ                | 10                | 11                   | 12                | 13               | 1.4<br>4.           |

| Sequence 2046, Ap<br>Sequence 5, Appli<br>Sequence 5, Appli<br>Sequence 14, Appl       | equence 12<br>Sequence 1<br>equence 21<br>equence 50<br>equence 8,                                  | Sequence 283, App<br>Sequence 33, Appl<br>Sequence 6, Appli<br>Sequence 8, Appli<br>Sequence 29, Appli<br>Sequence 7, Appli<br>Sequence 46, Appli | v in m in m in m                                                                                                                                   | 1862,<br>0 1112<br>0 31,<br>0 15,                                            |
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| 7.7. W.W.                                                                              | 25.12<br>25.15<br>25.15<br>25.25                                                                    | 12.3<br>12.3<br>12.3<br>12.7<br>111.7                                                                                                             | 11111111111111111111111111111111111111                                                                                                             |                                                                              |
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| 116<br>117<br>119                                                                      | 0 1 2 2 2 2 2 3 2 4 2 3 2 3 2 3 3 3 3 3 3 3                                                         | 333109876<br>332109876                                                                                                                            | 4 12 10 12 12 14 15 16 16 16 16 16 16 16 16 16 16 16 16 16                                                                                         | 0<br>4 4 4 4 4<br>11 52 50 4 10                                              |

## ALIGNMENTS

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US-09-759-584-48

Sequence 48, Application US/09759584

Sequence 48, Application US/09759584

Balent No. US20010014732A1

GENERAL INFORMATION:
APPLICANT: CAMMUE, BRUND P.A.
APPLICANT: CAMMUE, BRUND P.A.
APPLICANT: CAMMUE, BRUND P.A.
APPLICANT: TEREAS, FRANKE N.G.
APPLICANT: TEREAS, FRANKE N.G.
APPLICANT: TEREAS, FRANKE N.G.
APPLICANT: TEREAS, FRANKE N.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STATE: 1100 NEW YORK AVENUE, N.W.
STATE: 1100 NEW YORK AVENUE, N.W.
STATE: 100 OF COMPAIRED OF
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APPLICANT: Meloen, Robbert
APPLICANT: Puijk, Wouter
APPLICANT: Poijk, Wouter
APPLICANT: Broekaert, Wilhelmus
APPLICANT: Broekaert, Wilhelmus
APPLICANT: Nan Gelder, Wilhelmus
APPLICANT: Nan Gelder, Wilhelmus
APPLICANT: Rees, Sarah
FILLE OF INVENTION: Antifungal Proteins
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FILE OF INVENTION: 2003-094PDDIN
CURRENT APPLICATION WUMBER: US 09/077,948
PRIOR PILLING DATE: 1998-08-07
PRIOR PLILING DATE: 1996-07
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 ; Sequence 45, Application US/10388361A; Publication No. US20030226169A1
 APPLICANT: Van Amerongen, Aart
APPLICANT: Van Amerongen, Aart
APPLICANT: Borremans, Frans
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APPLICANT: Sitjtsma, Lolke
APPLICANT: Meloen, Robbert
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APPLICANT: Schaaper, Wilhelmus
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APPLICANT: Sneakeart, Willem
APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Rees, Sarah
TELEPHONE: 202-861-3000
TELEPAX: 202-822-0944
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 RESULT 2
US-10-388-361A-45
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LOCATION:
US-09-759-584-48
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US-10-006-252A-19
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Sequence 19, Application US/10006252A
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GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Recexer, Willem
APPLICANT: Recexer, Willem
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYR. 034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT PELLING DATE: 1998-06-10
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SEQ ID NOS: 77
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 NUMBER OF SEQ ID NOS: 141
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGIH: 414
PRIOR APPLICATION NUMBER: GB 9525455.3
PRIOR FILING DATE: 1995-12-13
 TYPE: DNA
ORGANISM: Raphanus sativus
 Matches 414; Conservative
 TYPE: DNA ORGANISM: Raphanus sativus
 Similarity
 US-10-388-361A-45
 US-10-006-252A-19
 Query Match
Best Local S
 361
```

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Query Match
Best Local Similarity 98.8
Matches 256; Conservative
 CURRENT APPLICATION DATA
 APPLICATION NUMBER:
FILING DATE:
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
 43..282
 Wilmington
 USA
 19850
 ; NAME/KEY:
; LOCATION:
US-09-759-584-58
 DE
 US-09-732-561-13
 COUNTRY:
 CITY: V
STATE:
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 61 GITCTITITGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
 181 AACCTIGAGAAAGCACGACAIGGAICTIGCAACTAIGICTICCCAGCICACAAGIGIAIC 240
 TGCTACTITCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTTATGTAATTAC 300
 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
09
 GIICTITITIGCIGCITITCGAAGCACCAACAATGCIGGAAGCACAGAAGTIGIGCGAAAGG 120
 241 IGCIACITICCITGITAATITAICGCAAACICITIGGIGAATAGTITITAIGIAATITAC 300
 GITITATIAGIGATCATGGCTAAGITIGCGTCCATCATCGCACTTCTTTTGCTGCTCTT 60
 361 GIIGGIICGGIIARACAARAAGIITIIAIICACCAAAAAAAAAAAAAAAA 414
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOPRATING SYSTEM: PC-DOS/MS-DOS
SOFWHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
 ATTORNEY/AGENT INPORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEB.36525/US/A
TELECOMMUNICATION:
TELEPHONE: 202-861-3000
TELEPRAK: 202-862-3094
 APPLICANT: CANUE, BRUNO P.A.
APPLICANT: CANUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, UOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
SOCRESPONDENCE ADDRESS:
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
 Sequence 58, Application US/09759584 Patent No. US20010014732A1 GENERAL INFORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
 FILING DATE:
CLASSIFICATION:
 STATE: D.C. COUNTRY: US ZIP: 20005
 US-09-759-584-58
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147
 61 GITCITITIGCIGCITICGAAGCACCAACAAIGGIGGAAGCACAGAAGIIGIGCGAAAGG 120
 148 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 207
 208 AGACTIGAGAAAGCACGACATGGATCTIGCAACTAIGTCTICCCAGCICAAAGGGTGTATC 267
 87
 88 drictititiecrecriticeaaccaccaacaarecrecaaccacaaagurgreccaaage
 1 GITTTATTAGTGATCATGGCTAAGTTTGCGTCCATCGCACTTCTTTTTGCTGCTCTT
 28 GITTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
 181 AACCITGAGAAAGCACGACAIGGAICITGCAACIAIGICITCCCAGCICACAAGIGIAIC
 ö
 Length 288;
 Indels
61.4%; Score 254.2; DB 9;
98.8%; Pred. No. 2.8e-58;
iive 0; Mismatches 3;
 Version #1.25
 APPLICANT: Thomma, Bart
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Kazan, Kemal
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS;
 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: 920 50165/UST
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
 US/09/732,561
 Sequence 13, Application US/09732561
Patent No. US20020035738A1
GENERAL INFORMATION:
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
 ADDRESSEE: ZENECA AG Products
STREET: 1800 Concord Pike
 241 TGCTACTTTCCTTGTTAAT 259
 268 recraciricerreria
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ö
 61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
 71 GTTTTCTTTGCTGCTCTTGAAGCACCGATGGTGGTGGAAGCACAGAAGTTGTGCGAGAGG
 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCAAGTGTATC 240
 191 AACCTTGAGAAAGCACGACGATGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATC 250
 241 TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
 251 rectacriteccarerrateraceaagacrerraargerraaraaagrergrarr 310
 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
 311 CTATTAAATAAGTATGTGTCACTCTATGAGAGGTCTTATGACATGTACCAGATATGTTAT 370
 09
 70
 1 GITITATIAGIGATCAIGGCIAAGITIGCGICCAICAICGCACTICITITIGCIGCICIT
 11 Graralacaragreargetralgreagetraceracerracerretretregeretr
 Gaps
 ;
0
 Query Match 58.6%; Score 242.4; DB 9; Length 403; Best Local Similarity 76.5%; Pred. No. 5e-55; Matches 297; Conservative 0; Mismatches 91; Indels 0
 MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 APPLICANT: Thomma, Bart
APPLICANT: Terras, Franky
APPLICANT: Terras, Franky
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Kazan, Kemal
APPLICANT: Brockeert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
 361 GTTGGTTCGGTTATACAAATAAAGTTTT 388
 371 Grigoringrinaaraaggraagcini 398
 APPLICATION NUMBER: US/09/732,561
FILING DATE:
CLASSIFICATION:
 Sequence 15, Application US/09732561
Patent No. US20020035738A1
GENERAL INFORMATION:
 SSEE: ZENECA Ag Products
1: 1800 Concord Pike
Wilmington
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS; single
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 TOPOLOGY: linear MOLECULE TYPE: cDNA ORIGINAL SOURCE: STRAIN: PDF 1.1
 CDNA
 USA
 19850
 ADDRESSEE:
 E
 ; STRAIN: F
US-09~732-561-13
 US-09-732-561-15
 COUNTRY:
 STREET:
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65 TITITIGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAA 124
 81 TCTTTGCTGCTTTCGACGCACCGGCAATGGTGGAAGCACAGAAGTTGTGCGAGAAGCCAA 140
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 201 IIGAAGGAĞCCAAACATĞĞATCATĞÇAACTATĞTCTTÖCCAĞĞACACAĞAĞTĞTATCTĞTT 260
 245 ACTITCCTIGITAAITITAICGCAAACTCTITGGIGAATAGITTTTAIGIAATTIACACAA 304
 261 ACGTCCCATGTTAAATCTACCACTAATCTTTGGTGCTAAATCGTGTGTATTTTACATAAA 320
 5 TATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTC 64
 21 TAATAATCATCATCATGGCTAAGTTTGCTTCCATCATCACCCTTATCTTCGCTGCTCTTGTTC 80
 Gaps
 ;
7
 APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: Zhu, T.
APPLICANT: Han, B.
APPLICANT: Wang, X.
APPLICANT: Wooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILS REFERENCE: 1360.001US1
 Query Match 53.9%; Score 223; DB 9; Length 400; Best Local Similarity 79.9%; Pred. No. 8.2e-50; Matches 274; Conservative 0; Mismatches 67; Indels
 305 AATAAGTCAGTGACTATCCATGAGTGATTTTAAGACATGTA 347
 321 AATAAGTCNCTGTCAC--TCTNTGAGTAACTTTATGACATGCA 361
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NUMBE: Hohenschutz, 112a D.
REGISTAATION NUMBER: 33,712
REPERENCE/DOCKET NUMBER: PPD 50165/UST
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 15:
 CURRENT APPLICATION NUMBER: US/09/887,576 CURRENT FILING DATE: 2001-06-25
 CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR PLIUGATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692
 Sequence 607, Application US/09887576
Patent No. US20020144047A1
 APPLICATION NUMBER: 09/202,638 FILING DATE:
 SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
 single
PRIOR APPLICATION DATA:
 APPLICANT: Budworth, P.
 MOLECULE TYPE: CDNA ORIGINAL SOURCE: STRAIN: PDF1.2
 linear
 GENERAL INFORMATION:
 STRANDEDNESS:
 -09-887-576-607
 US-09-732-561-15
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Query Match
Best Local Similarity
 121
 Query Match
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 244
 65 TITITIGCIGCITITCGAAGCACCAACAAIGGIGGAAGCACAGAAGITGIGCGAAAGGCCAA 124
 81 TCTTTGCTGCTTTCGACGCACCGCAATGGTGGAAGCACAGAAGTTGTGCGAGAAGCCAA 140
 GTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACC 184
 245 ACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTACACAA 304
 261 Acgrecearcriaarcraecacraarcririderecraarcererererriracaraaa 320
 21 TAATAATCATCATGGCTAAGTTTGCTTCCATCATCACCCTTATCTTCGCTGCTCTTGTTC 80
 5 TATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTC 64
 NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
 185 ITGAGAAAGCACGACATGTTGCAACTATGTCTTCCCAGGCTCACAAGTGTATCTGCT
 Gaps
 5
 Rosenberger, Cindy A.
INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
 Length 400;
 ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION APAR:
APPLICATION NAME: 09/103,489
FILING DATE: 1998-06-24
 67; Indels
 305 AATAAGTCAGTGTCCATGAGTGATTTTAAGACATGTA 347
 321 AATAAGTCNCTGTCAC--TCTNTGAGTAACTTTATGACATGCA 361
 Score 223; DB 9;
Pred. No. 8.2e-50;
0; Mismatches 67;
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 607
LENGTH: 400
 Sequence 16, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
 TYPE: DNA ORGANISM: Arabidopsis thaliana
 Query Match
Best Local Similarity 79.9%;
Matches 274; Conservative
 ; LOCATION: (1).T. (400)
; OTHER INFORMATION: n = A,T,C
US-09-887-576-607
 NAME/KEY: misc_feature
LOCATION: (1)...(400)
 TITLE OF
 RESULT 8
US-09-829-381A-16
 125 (
 FEATURE
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APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: W. Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for CO TITLE OF INVENTION: Plant Pathogenic Pungi
TITLE OF INVENTION: Plant Pathogenic Pungi
TITLE OF INVENTION: Plant Pathogenic Pungi
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT PILING DATE: 2001-04-09
PRIOR FILING DATE: 2001-04-09
PRIOR PELICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOUTHARE: Patentin version 3.1
SEQ ID NO 16
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 135
 180
 240
 196 AACCTCGAGAAGGCACGGCATGGATCTTGCAACTACGTCTTCCCAGCTCACAAGTGCATC 255
 61 GITCITITIGCIGCITICGAAGCACCAACAAIGGIGGAAGCACAGAAGITGTGCGAAAGG 120
 75
 16 GITTIATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTCTTTGCTGCTCTTC
 76 Gricicirirecrecificasecaccaacrarecreeaecacaaaacricreceaeaee
 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
 1 GITITATIAGIGATCAIGCTAAGIIIIGCGICCAICAICGCACIICIIIIIGCIGCICII
 Gaps
 ö
 Length 285;
 52.9%; Score 219; DB 9; Length 285; 90.3%; Pred. No. 8.2e-49; ive 0; Mismatches 25; Indels
 NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6624
TELEPHONE: (314) 537-6647
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Score 219; DB 13;
Pred. No. 8.2e-49;
 TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA" SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 Sequence 16, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
 241 TGCTACTTTCCTTGTTAAT 259
 256 IGCTACTITCCAIGCTAAT 274
ATTORNEY/AGENT INFORMATION:
 TYPE: DNA ORGANISM: Artificial Sequence
 52.9%;
 ; OTHER INFORMATION: Synthetic US-10-681-972-16
 Best_Local Similarity 90.3
Matches 234; Conservative
 US-09-829-381A-16
 US-10-681-972-16
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AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240

255

120

9 75

Gaps

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Indels

Pred. No. 5.9e-48;

89.68;

0; Mismatches

1 GITITATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT

180

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 61 GTTCTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
 16 GITTTATTAGGGALCATGGCTAAGTTTGCGTCCATCGCACCCCTCTTTGCTGCTCTC
al Similarity 89.6
232; Conservative
 181
 16
 Best Local &
Matches 232
 Best Loca
Matches
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 AACCITGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGGTCACAAGTGTATC 240
 120
 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 136 ccarcadedacridercadeadricrecedaadcaacaacearecaagaaccaarecare 195
 196 AACCICCAGAAGGCACGGCAIGGAICTIGCAACIACGICTICCCAGCICACAAGIGCAIC 255
 9
 75
 CORRESPONDENCE ADDRESS:
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
 1 GITITATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTT
 16 GITITATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTCCTCTTTGCTGCTCTC
 61 GITCITITIGCIGCITITCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
 Gaps
 ..
0
 Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
 Length 285;
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PAC-DOS/MS-DOS
SOFTWARE: PAC-DOS/MS-DOS
TILING DATE: 09-Appr-2001
CLASSIFICATION NUMBER: US/09/829,381A
FILING DATE: 09-Appr-2001
CLASSIFICATION CUMCOMP.
PRIOR APPLICATION DATA:
 25; Indels
 DB 9;
 NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEPAX: (314) 537-6047
 MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-829-381A-17
 0; Mismatches
 52.1%; Score 215.8;
 APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
 APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal P.
 Sequence 17, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
 TGCTACTTTCCTTGTTAAT 259
 recracrirecarecraar 274
 LENGTH: 285 base pairs
 INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
STRANDEDNESS: single
 TOPOLOGY: linear
 234; Conservative
 NUMBER OF SEQUENCES:
 COUNTRY: USA
 US-09-829-381A-17
 121
 181
 241
 256
 Matches
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ALYAFP from Alyssum and Methods for Control
 61 GITCITTITGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
 240
 136 CCATCAGGACTTGGTCAGGAGTCTGCGGAAACAACAACGCATGCAAGAACCAATGCATG 195
 75
 1 GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTT
 16 GITTIATIAGIGAICAIGGCIAAGITIGCGICCAICAICGCCACCCCTCIIGGCIGCTC
 76 GTTCTCTTTGCTGCTTTTCGAGGCACCACTATGGTGGAGGCACAAAAGTTGTGCCAAAGG
 181 AACCITGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGGTCACAAGTGTATC
 Gaps
 0
 285;
 Length
 Indels
 DB 13;
 y Match 52.1%; Score 215.8; DB 13; Local Similarity 89.6%; Pred. No. 5.9e-48; hes 232; Conservative 0; Mismatches 27;
 Sequence 17, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
ITILE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C.
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT APPLICATION NUMBER: US/09/829,381D
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOGTWARE: Patentin Version 3.1
SEQ ID NO 17
 241 TGCTACTTTCCTTGTTAAT 259
241 TGCTACTTTCCTTGTTAAT 259
 274
 256 recracrirecarecraar
 TYPE: DNA ORGANISM: Artificial Sequence
 OTHER INFORMATION: Synthetic
 -10-681-972-17
 US-10-681-972-17
 Query Match
 FEATURE:
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Query Match

요

```
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
ITIE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for CO.
ITIE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C.
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 500
 AGATATGTTAT-----GTTGGTTCGGTTATACAATAAAGTTTTATTCACCAA 397
 290 ATGTAATTTACACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC
 359 TGTTTATTTACATGAAATAAGTCTGTGTCA-TCCTTATGGGTGACCTTATGACATGTACC
 359 IGTTTATTACATGAAATAAGTCTGTGTCA-TCCTTATGGGTGACCTTATGACATGTACC
 66 ITITIGCIGCITICGAAGACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAG
 119 crindciectriricaAscaccascaArcardaAsGTCACGGAAGTTGTGCGAGAGTCCAAG
 126 TGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCT
 TGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTA
 CTTTCCTTGTTAATTTATCGCAAACTCTTTGGTG------AATAGTTTTT
 cricccardria archacca a a carrirre recorde recordina rec
 290 ATGTAATTTACACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC
 59 AGTAATAGATATGGCTAAGTGTGCTTCCATCATCTCCCTTGTCTCTGCTGCTCTTGTTCT
 179 TGGAACATGGTCAGGCGTGTGTGGGAATAATAATAACGCATGCAGGAACCAATGCAGAAACCT
 239 TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA
 Gaps
 29;
 Ouery Match
49.1%; Score 203.4; DB 13; Length 500;
Best Local Similarity 72.5%; Pred. No. 1.7e-44;
Matches 317; Conservative 0; Mismatches 91; Indels 29;
 6 ATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACT
 NAME/KEY: misc_feature

1 LOCATION: (22)...(22)

2 OTHER INFORMATION: N = any nucleotide

US-10-681-972-9
 Sequence 9, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
 398 AAAAAAAAAAAAAA 414
 TGCAAAAAAAAAAAA 494
 TYPE: DNA
ORGANISM: Alyssum spp
FEATURE:
 RESULT 13
US-10-681-972-9
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 418
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 186
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 AGTAATAGATATGGCTAAGTGTGCTTCCATCATCTCCCTTGTCTCTGCTGCTCTTGTTCT 118
 TGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCT 185
 redaacarecraegecererereseaaraareecarecraecaarecraeaaacer 238
 245
 TITIGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAG 125
 119 criridoridoririnda a de decado d
 246 CTTTCCTTGTTAATTTTATCGCAAACTCTTTGGTG---------AATAGTTTTT 289
 9
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
 TGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGGCTCACAAGTGTATCTGCTA
 6 ATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCT
 Gaps
 APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
 29;
 49.1%; Score 203.4; DB 9; Length 500; 72.5%; Pred. No. 1.7e-44; Live 0; Mismatches 91; Indels 29
 COMPUTER FOLDS.

COMPUTER FOLDS.

MEDIUM TYPE: Floppy disk
COMPUTING SYSTEM: FLOWER COMPATING
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION ADMR:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTOWNEY/AGENT INFORMATION:
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A
 NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
 7 TOPOLOGY: linear

7 MOLECULE TYPE: cDNA

7 SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-829-381A-9
 Sequence 9, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
 LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Best Local Similarity 72.5
Matches 317; Conservative
 NUMBER OF SEQUENCES:
 CITY: St. Louis
STATE: Missouri
 COUNTRY: USA
 ZIP: 63198
 RESULT 12
US-09-829-381A-9
 59
 99
 179
 186
 239
 126
 Query Match
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118 125 178 185 238 245 298 289

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65

349 358

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Sequence 2046, Application US/09938842A
; Sequence 2046, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Wreps, Joe1

APPLICANT: Wreps, Joe1

APPLICANT: Wreps, Joe1

APPLICANT: Mang, Xun

APPLICANT: Sane, AND METHODS OF PLANTS, TRANSGENIC FLANTS CONTAINING

TITLE OF INVENTION: SARE, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-6-22

NUMBER OF SEQ ID NOS: 5379

LENGTH: 243
 Sequence 2046, Application US/09938842A
Publication No. US20040009476A9
GUNEAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harper, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
 ô
350 AGATATGTTAT-----GTTGGTTCGGTTATACAAATAAAGTTTTATTCACCAA 397
 418 AGATATATCATATATGTATGTTGTTTGTTGTGTGGCAATTATAAACTTTTATTTGTGGA 477
 121 TCAGGGGTTTGCCGGAACAGTAATGCATGCAAGAATCAGTGCATTAACCTTGAAGGAGCC 180
 76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAAGTGGGACATGG 135
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 196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
 181 AAACATGGATCATGCAACTATGTCTTCCCAGCACAAGTGTATCTGTTACGTCCCATGT 240
 1 Argecraagringcinccarcarcarcarcinarcincecrecingricicinischeci 60
 16 ATGCCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTGCTGCT
 tch 47.5%; Score 196.6; DB 9; Length 243; al Similarity 88.1%; Pred. No. 8e-43; 214; Conservative 0; Mismatches 29; Indels 0;
 398 AAAAAAAAAAAAAA 414
 478 TGCAAAAAAAAAAAA 494
 ORGANISM: Arabidopsis thaliana
 Query Match
Best Local Similarity
Matches 214; Conserv
 TAA 258
 TAA 243
 RESULT 14
US-09-938-842A-2046
 RESULT 15
US-09-938-842A-2046
 US-09-938-842A-2046
 TYPE: DNA
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61 TTCGACGCACGCAATGGTGGAAGCACAGAAGTTGTGCGAGAAGCCAAGTGGGACATGG 120
 76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
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 75
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88.1%; Pred. No. 8e-43;
tive 0; Mismatches 29; Indels 0;
 CURENT FILING NUMBER: US/09/938,842A
CURENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
LENGTH: 243
 completed: May 13, 2004, 11:00:39
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FILE REFERENCE: SCRIP1300-3
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Matches 214; Conservative
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 241 TAA 243
 US-09-938-842A-2046
 Search completed: Ma
Job time : 341 secs
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CD833779 BN46.0031
CD834411 BN45.041
CD834411 BN45.041
CD833024 BN40.058N
CD833024 BN40.058N
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CD8332298 BN45.062B
 CD834994 10-JUL-2003 RRNA linear EST 10-JUL-2003 BN45.043006F011229 BN45 Brassica napus CDNA clone BN45043006, RRNA
 Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 458)
Genoplante.
 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infoblogen.fr).
 program in plant genomics
 Genoplante, a major partnership french
Unpublished (2003)
Contact: Genoplante
Genoplante
 ALIGNMENTS
 CD832625
CD834168
CD833977
CD837517
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CD834090
 CD833628
CD833627
 CD829085
 CD831014
 AV787956
 CD834994.1 GI:32516934
 Brassica napus (rape)
 \begin{array}{c} \mathcal{C} \wedge \mathcal{
 sequence.
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 1
CD834994
LOCUS
DEFINITION
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 REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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CD832071 BN40.0610
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 55026578
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 27513289 segs, 14931090276 residues
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 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 CD834994
CD831680
CD834068
CD832071
 nucleic search, using sw model
 IDENTITY_NUC Gapop 10.0
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414
 seq length: 0
seq length: 200000000
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Query
Match Length DB
 EST:*
 75.8
75.2
75.1
75.1
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311
311
 Perfect score:
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 Score
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 Total number
 Minimum DB
Maximum DB
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 Database
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Best Local Similarity 89.7
Matches 357; Conservative
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 DEFINITION
 AUTHORS
TITLE
JOURNAL
 REFERENCE
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 RESULT 3
CD834068
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 CD831680 470 bp mRNA linear EST 10-JUL-2003
BN40.060H13F011227 BN40 Brassica napus cDNA clone BN40060H13, mRNA
 Grafitaciadreadedreaderriectricearcarececeeerrifitaereceeerriecteerrie 110
 GTTCTTTTTGCTGCTTTTCGAAGCACCACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGG 120
 GITCITITICGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAGAGG 170
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 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
 ATAAAATAAGTCTGTGTCACTATCAATGAGTGATTTTATGACATGTACCTGATATATGTT 410
 Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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 1 GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT 60
 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
 Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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 Brassica napus (rape)
Brassica napus
 75,8%;
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Conservative
 Contact: Genoplante
Genoplante
 Similarity
 Genoplante.
 CD831680
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Matches 362;
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CD831680
LOCUS
DEFINITION
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 ACCESSION
VERSION
KEYWORDS
SOURCE
 AUTHORS
TITLE
 JOURNAL
COMMENT
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CD834068 446 bp mRNA linear EST 10-JUL-2003
BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA
 GIATIACIAGIGAGCAIGGCIAAGITIGCIICCAICAITGCCCCCACTITIIGCIGCICII 132
 133 gircirircecrecrircaaagcaccaacaaregregaagcacagaagtrereceagaaga 192
 253 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATT 312
 373 ATAAATTAAGTCTGTGTCACTATCAATGAGTGATTTTATGACATGTACCTGATATATGTT 432
 GITCITITIGCTGCTITCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 193 ccaagregeacaregercagagercreregaaacaaraaacecarecaagaarcagreerr 252
 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
 241 IGCIACTITICCITGITAATITIAICGCAAACTCITIGGTGAATAGITITITATGTAATITAC 300
 313 recracircecirerraacrianeeeaaacreirreereerracrirererarirae 372
 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
 09
 Tracheophyta;
 73. rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
 Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
 GITITATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 ω
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 Length 470;
 Indels
 396
 Argriggircggriara-araaaagrirrargcacca 469
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 38;
 AIGTIGGITCGGITATACAAATAAAGITTTATICACCA
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/mol_type="mRNA"
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 /db_xref="taxon:3708"
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EST.
 75.2%;
89.7%;
 Brassica napus (rape)
 (bases 1 to 446)
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CD835064 10-JUL-2003 BN45.044C21F011228 BN45 Brassica napus CDNA clone BN45044C21, mRNA
 Brassica napus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spernatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
1 (bases 1 to 519)
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 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
 355 ATAAAATAAGTCTGTGTCACTATGAATGAGTGATTTTATGACATGTACCTGATATATGTT 414
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
 program in plant genomics
 GTTCTTTTCGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAGAGG
 235 AACCTTGAGAAAGCACGACATGGATCTTGCAATGTCTTCCCAGCTCACAAGTGTATT
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 175 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
 AACCTTGAGAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
 51 Grannachárica geargeorna ar mhachrachta richtach a chainn a cha
 GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
 295 IGCTACTICCCTIGITAACTIAIGCGCAAACTCTTIGGTGGTTAGTTTTGTGTAATTTAC
 1 GITITATIAGIGATCAIGGCIAAGTITGCGICCAICAICGCACTICTITIGCIGCICTI
 Gaps
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 75.0%; Score 310.6; DB 14; Length 519;
Larity 86.4%; Pred. No. 2.6e-41;
Conservative 0; Mismatches 54; Indels 2;
 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
 Genoplante, a major partnership french
Unpublished (2003)
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| /organism="Brassica napus"
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 CD835064.1 GI:32517004
 Brassica napus (rape)
 Contact: Genoplante
 Genoplante.
 Local Similarity
nes 355; Conserv
 sequence.
CD835064
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 EST.
 55
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 181
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 359
 Н
 61
 121
 Query Match
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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COMMENT
 REFERENCE
AUTHORS
 RESULT 5
CD835064
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 UD832071 452 bp mRNA linear EST 10-JUL-2003
BN40.061003F011227 BN40 Brassica napus CDNA clone BN40061003, mRNA
sequence.
 ij,
 110
 180
 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 230
 358
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, sosids, eurosids II; Brassicales, Brassicaceae, Brassica.

(bases 1 to 452)
 111 GITCITITCGCIGCITICGAAGCACCAACAAIGGIGGAAGCACAGAAGITGIGCGAGAGG 170
 AACCTIGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
 TGCTACTTTCCTTGTTAATTTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
 291 recracificectricitalectratececaaecretricerecracificateralizativae 350
 9
 Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
191, rue Henri Rochefort 91025 EVRY CEDEX France
Pax: 33 1 69 47 54 00
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATT
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 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
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 351 ATAAAATAAGTCTGTGTCACTATGAATGAGTGATTTTATGACATGTACCTGATATGTT
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Score 311, DB 14; Length 446;
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0; Mismatches 40; Indels 2
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cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="RNAf0061003"
/tissue_type="seed"
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 Arcriccrircraraaaaacrir 439
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Query Match
Best Local Similarity 89.2%;
Matches 347; Conservative
 Brassica napus (rape)
 Brassica napus
 Genoplante.
 241
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 301
 411
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VERSION
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CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
 5,
 Score 309.4; DB 14; Length 408; Pred. No. 4.8e-41; 0; Mismatches 41; Indels 2;
 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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88.9%;
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Best Local Similarity 88.9
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 sequence.
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SOURCE
ORGANISM
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TITLE
JOURNAL
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CD833779
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 CD822592 447 bp mRNA linear EST 10-JUL-2003 BN40.063015F011228 BN40 Brassica napus cDNA clone BN40063015, mRNA
 109
 GTTCTTTTCGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGGGAGAGG 170
 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGGTCACAAGTGTATT 290
 TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
 291 recractroccriorraacriarececaaacreirresresrasirricroraaaricae 350
 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
 351 ATAAAATAAGTCTGTCACTATCAATGAGTGATTTTATGACATGTACCTGATATATGTT 410
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 GTTCTTTTTGCTGCTTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
 Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
 GTTCTTTTCGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAGG
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 74.9%; Score 310; DB 14; Length 447; 88.9%; Pred. No. 3.6e-41; ive 0; Mismatches 41; Indels 5
 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Brassica napus
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 346;
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 LOCUS
 REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
 Matches
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 RESULT 6
CD832592
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CD833779 408 bp mRNA linear EST 10-JUL-2003
BN45.001115F010914 BN45 Brassica napus cDNA clone BN45001115, mRNA
 240
 409
 120
 349
 73 GITCITITCGCIGCITICGAAGCACCAACAATGGIGGAAGCACAGAAGITGTGCGAGAGG 132
 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
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 ACAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
 Streptophyta; Embryophyta; Tracheophyta;
 72
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
 Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
 61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
 290 recracificeciral de la reconsta del la reconsta de la reconsta
ccaaginggacargercaggagicrgrggaaacaaraacgcargcaagaarcagrgcarr
 AACCITGAGAAAGCACGACATGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
 350 ATAAAATAAGTCTGTGTCACTATCAATGAGTGATTTTTATGACATGTACCTGATATATGTT
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 Brassica napus
Makaryota; Viridiplantae, Streptophyta, Embryophyta, Tracheor
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids, II, Brassicales, Brassicaceae, Brassica.
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CD834611
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 Brassica napus (rape)
Brassica napus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, euroside II; Brassicales, Brassicaceae, Brassica
 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
 314 ATAAAATAAGTCTGTCTCACTATCAATGAGTGATTTTATGACATGTACCTGATATGTT 373
 Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
 TGCTACTITCCTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC
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 61
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CD834611
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 UD834090 405 TIO-UUL-2003 BN45.040121F011018 BN45 Brassica napus CDNA clone BN45040121, mRNA sequence.
 240
 TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTTAC 300
 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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 181 AACCTIGAGAAAGGACGACAIGGAICTIGCAACTAIGICTICCCAGCICAGAGIGIAIC 240
 Contract: Genoplante
Genoplante
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Genoplante
19, 724 169 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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 73
 Genoplante, a major partnership french program in plant genomics Unpublished (2003)
AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
 ACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATT
 14 GTATTACTAGTGAGCATGGCTAAGTTTGCTTCCATCATTGCCCACTTTTTGCTGCTCTT
 74 GIICITITICGCIGCITITICGAAGCACCAACAATGGIGGAAGCACAGAAGTIGIGCGAGAG
 1 GITITATIAGIGATCAIGGCIAAGITIGCGICCAICAICGCACTICITITIGCIGCICIT
 Gaps
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 Length 409;
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 74.7%; Score 309.4; DB 14;
88.9%; Pred. No. 4.7e-41;
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 359
 121
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Gaps ., 110 120 170 180 230 240 290 300 350

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 sednence.
 396 GTT 398
361 GTT 363
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 GTT 397
 CD833944
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 DEFINITION
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CD833944
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 CD831294 110-JUL-2003 818 bp mRNA linear EST 10-JUL-2003 BN40.058N13F011019 BN40 Brassica napus cDNA clone BN40058N13, mRNA
 ·.
 Brassica napus
Brassica napus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
 351 ATAAAATAAGTCTGTGTCACTATCAATGAGTGTTTTTATGACATGTACCTGATATATGTT 410
301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
 61 GITCITITIGCIGCITICGAAGCACCAACAATGGIGGAAGCACAGAAGTIGIGCGAAAGG 120
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 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTAT 360
 336 ATAAAATAAGTCTGTGTCACTATCAATGAGTGATTTTATGACATGTACCTGATATGTTAT 395
 36 diainachaghdahdahdachadhhhachhcahdahnacachachhnhachachdh 95
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr)
 Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
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 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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 411 Argrirgerirgerirarahahaharrir 439
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CD833944 420 Dp mRNA linear EST 10-JUL-2003 BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
 Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
 155 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 214
 61 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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 275 TGCTACTTCCCTTGTTAACTTATGCGCAAACTCTTTGGTGGTTAGTTTTGTGTAATTTAC 334
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 94
 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
 Genoplante, a major partnership french program in plant genomics Unpublished (2003)
 1 GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
 35 Grarracragicarcareecraagrirecriccareariececracririrecrecie
 0; Gaps
 Query Match 74.2%; Score 307; DB 14; Length 420; Best Local Similarity 90.4%; Pred. No. 1.1e-40; Matches 328; Conservative 0; Mismatches 35; Indels (
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CD833983
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 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCAAGTGTATC 240
 276 İGCIACİİCCCİİĞİTAACİİAİGCGCAAACICİTİTĞGIGGİTAGİTİTĞGIAALİTİAC 335
 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infoblogen.fr),
Location/Qualifiers
 Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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 1 GITITATIAGIGATCAIGGCIAAGITIGCGICCAICAICGCACTICITITIGCIGCICTI
 96 drechrinescriscrecedadeacacacaarastastascacacaaaathstassaaass
 156 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
 336 ATAAAATAAGTCTGTGTCACTATCAATGAGTGATTTTTATGACATGTACCTGATATGTTAT
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Brassica napus
 Contact: Genoplante
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 398
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 Query Match
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KEYWORDS
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CD827413
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 EST 10-JUL-2003
BN25064A05, mRNA
 Brassica napus (rape)
Brassica napus
Brassica napus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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 61 GITCITITIGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG 120
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 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
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 AACCTIGAGAAAGCACGACAIGGAICTIGCAACTAIGICTICCCAGCICACAAGIGIAIC 240
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 92
 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 00
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
 Genoplante, a major partnership french program in plant genomics Unpublished (2003)
 36 GTATTACTAGTGATCATGGCTAAGTTTGCTTCCATCATTGCCCTACTTTTGCTGCTCTT
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 156 CCAAGTGGGACATGGTCAGGAGTCTGTGAACAATAACGCATGCAAGAATCAGGGCATT
 TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC
 Gaps
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 Query Match

74.2%; Score 307; DB 14; Length 421;
Best Local Similarity 90.4%; Pred. No. 1.1e-40;
Matches 328; Conservative 0; Mismatches 35; Indels (
 BN25.064A05F020416 BN25 Brassica napus cDNA clone sequence.
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 Contact: Genoplante
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Gaps

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360 395 CD827413 426 bp mRNA linear BST 10-JUL-2003 MSDS.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA cD827413 LOCUS DEFINITION ACCESSION

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 CD831479 438 bp mRNA linear EST 10-JUL-2003 BN40.059J13F011208 BN40 Brassica napus cDNA clone BN40059J13, mRNA
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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 93, rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10 Fax: 31 69 47 54 10 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr)
 Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Brassica.

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 plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr),
 Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
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